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APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: REES, Michael A.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURPACE RESIDUE VENEERING OF RODENT
TITLE OF INVENTION: ANTIBODIES;
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughtue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pensylvania Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 109;
Sequence 2, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: RABES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
APPLICANT: GUILD, Braydon C.
APPLICANT: GUILD, BRAYDON C.
APPLICANT: MICHAEL A.
APPLICANT: GUILD, BRAYDON C.
APPLICANTION: SURFACE RESIDUE VENEERING OF RODENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.3%; Score 33; DB 1; Length 109
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                       ADDRESSE: Sughrue, Mion, Zinn, Macpeak & Seas STREFT: 2100 Pensylvania Avenue, N.W. CITY. Washington STATE: D.C. COUNTRY: United States ZIP: 20037-3202 COMPUTER READABLE FORM: MEDIUM TYPE: H P 9000/700 Workstation OPERATING SYSTEM: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION: 1NFORMATION:
TELEPRAX: (202) 293-7060
TELEFAX: (4091103
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 10, Application US/07942245; Patent No. 5639641
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STATE: D.C.
COUNTRY: United States
7TP: 20037-3202
                                                                                               APPLICANT: SEARLE, STEE
APPLICANT: REES, Ant.
APPLICANT: ROGUSKA, Mic.
APPLICANT: GUILD, Brat
TITLE OF INVENTION: SURF.
TITLE OF INVENTION: ANTI.
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-2
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US-07-942-245-10
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825 TPTLIGGGAI 834
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                                                                                                 US-09-240-274-38
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 38
LENGTH: 107
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Patent No. 6448234

GENERAL INFORMATION:
APPLICANT: Steven P. Fling

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 179, Application US/09598419
Fatent No. 656556
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT APPLICANTION: COMPOUNDS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: LAGGOC
GURRENT APPLICATION WUMBER: US/09/598,419
CURRENT FILIAD DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                   64.2%; Score 34; DB 4; Length 1776; 60.0%; Pred. No. 1.4e+03; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.2%; Score 34; DB 4; Length 1776; 60.0%; Pred. No. 1.4e+03; Live 2; Mismatches 2; Indels
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CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
CURRENT FILING DATE: 3000-07-20
SOFTWARE: OF SEQ ID NOS: 363
SOFTWARE: FASTSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                       Local Similarity 60.0
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Matches 6; Conservative
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825 TPTLIGGGAI 834
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                                                                                                          LENGTH: 1776
TYPE: PRT
ORGANISM: Chlamydia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 45
US-09-620-412C-179
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LENGTH: 1776
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                                                                                                                                                                                                                       Query Match
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Sequence 39, Application US/09240274

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: RAID BINDING PROTEINS AND MACNETICALLY ACTIVATED CELL.

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE PREFERENCE: 05596-4202

CURRENT APPLICATION NUMBER: 05/0940,274

CURRENT RILING DATE: 1999-01-29

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 224
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                                          FACELLY NO. 0253123.

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: RAID)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT PELLCATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/081,500
EARLIER PILING DATE: 1998-04-10
EARLIER PILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER PILING DATE: 1098-04-10
EARLIER PILING DATE: 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 62.3%; Score 33; DB 3; Length 107
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: anti-Rh(D) chain I07
US-09-240-274-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: anti-Rh(D) chain 108 US-09-240-274-39
; Sequence 38, Application US/09240274
; Patent No. 6255455
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.00
Pest 6; Conservative
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US-07-942-245-2 RESULT 49

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154 PTVAGGGAL 162
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                                                       RESULT 43
US-09-072-967-204
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TUBERCULOSIS
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APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.2%; Score 34; DB 4; Length 943; ilarity 66.7%; Pred. No. 7.6e+02; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: ELOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILLING DATE: 05-MAY-1998
CLASSIFICATION:
            NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 4; I
Pred. No. 7.6e+02;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TILE REFERENCE: 52888

CURRENT APPLICATION NUMBER: US/09/477,135A

CURRENT PILING DATE: 2000-01-03

PRIOR APPLICATION NUMBER: US 96/10375

PRIOR PILING DATE: 1997-12-15

PRIOR PILING DATE: 1996-06-14

PRIOR PILING DATE: 1996-06-15

PRIOR PILING DATE: 1995-06-15

PRIOR PILING DATE: 1995-06-15

NUMBER OF SEQ ID NOS: 169

SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (2006) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-477-135A-131
; Sequence 131, Application US/09477135A
; Patent No. 6572865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECTOR. (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7%
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                                                                                                               Washington
FITTE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                        USA
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                                                                                                                                    COUNTRY:
                                                                                                               STATE:
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and not compounded.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Probet, Peter
APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Fling, Steve
APPLICANT: Fling, Steve
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL, INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 4; Length 943;
Pred. No. 7.6e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072.967
                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US/09/072,967
05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 98104-7092
COMPUTER READALLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Sequence 179, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
Sequence 204, Application US/09072967; Patent No. 6592877
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210121.469C5
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amino acid
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Best Local Similarity 66.7
Matches 6; Conservative
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Patent No. 6448234
GENERAL INFORMATION:
TELEMERAL INFORMATION:
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TILLE REFERENCE: 210121.46950;
TILLE REFERENCE: 210121.46950;
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 195
INDICT: 2010
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    APPLICANT: Fing, Steve
APPLICANT: Maisonneuve, Jeff
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C5
CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 195, Application US/09598419
Faterin Wo. 6565866
GENERAL INFORMATION:
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: LA6966
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT TILLS DATE OF SEQ ID NOS: 357
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 195
LIENGTH: 821
                                                                                                                                                                                                                                                                                                                                                               64.2%; Score 34; DB 4; Length 821; 60.0%; Pred. No. 6.7e+02; tive 2; Mismatches 2; Indels
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Best Local Similarity 60.0
Matches 6; Conservative
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Matches 6; Conservative
Skeiky, Yasir
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812 TPTLIGGGAI 821
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                                                                                                                                                                                                                                                                                              ORGANISM: Chlamydia
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; ORGANISM: Chlamydia
US-09-598-419-195
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APPLICANT:
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                                              Gaps
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
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Query Match

64.2%; Score 34; DB 4; Length 821;
Best Local Similarity 60.0%; Pred. No. 6.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PLICATION UNBER: US/09/056,556
FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                            3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                         ; Sequence 204, Application US/09056556; Patent No. 6350456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6458366
GENERAL INFORMATION:
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Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hendrickson, Ronald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4900
TELEPAX: (206) 622-631
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky, Yasir A.W.
Dillon, Davin C.
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TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 66.73
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                        812 rPTLIGGGAI 821
                                                                                  1 TPRVTGGGAM 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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ZIP: 98104-7092
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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US-09-056-556-204
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US-09-072-596-199
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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Query Match
Best Local Similarity 60...
G: Conservative
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Matches 6, Conservative
                                                                       258 rPTLIGGGAI 267
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                                1 TPRVTGGGAM 10
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                                                                                                                                                                                                                             GENERAL INFORMATION:
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US-09-252-991A-25715
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APPLICANT:
MARC J. Rubenfield et al.
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
RRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 33084
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Patent No. 6448234
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
CURRENT APPLICATION UNBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FARESEQ FOR WINDOWS VERSION 3.0/4.0
                                                                                                                                                                                                                                    Query Match

64.2%; Score 34; DB 1; Length 375;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Pseudomonas aeruginosa
TELECOMMUNICATION INFORMATION:
           TELEPHONE: (716) 856-4000
TELEPAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Chlamydia trachomatis
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Matches 6; Conservative
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                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-736-361A-5
                                                                                                                                                                                                                                                                                                                                                                       341 PRVTSGGS 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 PRTAGGGA 174
                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                           2 PRVTGGGA 9
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US-09-252-991A-33084
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LENGTH: 683
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 52115
LENGTH: 717
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                                                               APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENITON: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENITON: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REPERENCE: 210121.469C6
CURRENT PELLING DATE: 2000-06-20
NUMBER OF SEQ. ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.2%; Score 34; DB 4; Length 717; 75.0%; Pred. No. 5.9e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ' Sequence 25715, Application US/09252991A
' Patent No. 6551795
Sequence 357, Application US/09598419
Patent No. 6565856
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Patent No. 6432916
GENERAL INFORMATION:
APPLICANT: Probst, Peter
APPLICANT: Bhatia, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Chlamydia trachomatis
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GENERAL INCORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT PRILIGATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 24996
LENGTH: 344
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                                                                                                                                      0; Gaps
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                                                                                        Score 34; DB 4; Length 247;
Pred. No. 2.2e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Hodgson, Russ, Andrews, Woods & Goodyear
1800 One M&T Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wilson, David B.
APPLICANT: Lao, Guifang
TITLE OF INVENTION: Nucleotide Sequences encoding a
TITLE OF INVENTION: Thermostable Alkaline Protease
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPTRY: New LOLA
COUNTRY: New LOLA
COMPUTRY: READABLE FORM:
MEDIUM TYRE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
SOFTWARE: Wordperfect for Windows
SOFTWARE: Wordperfect for Windows
FULICATION UNDERS: US/08/736,361A
FILING DATE: 23 October 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.2%; Scor. No. 5co. 85.7%; Pred. No. 5co. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18617.0031
                                                                                                                                                                                                                                                                                                                                     Sequence 24996, Application US/09252991A Patent No. 6551795
  ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-414-828A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 5, Application US/08736361A; Patent No. 5705379
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
                                                                                          64.2%;
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                                                                                   Query Match
Best Local Similarity 75.0°
Matches 6; Conservative
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Best Local Similarity 85.77
6; Conservative
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                                                                                                                                                                                                                                                                                                              US-09-252-991A-24996
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US-08-736-361A-5
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APPLICANT: Plinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develo
             APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGIAINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196 136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24671
LENGTH: 1150
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Pred. No. 80;
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Sequence 14, Application US/09414828A

Patent No. 6300084

GENERAL INFORMATION:
APPLICANT: Drubin, David G.
APPLICANT: Hofmann, Christian J.
CURRENT APPLICATION: MUMBER: US/09/414,828A

CURRENT FILING DATE: 1998-10-06

PRIOR FILING DATE: 1998-10-08

NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
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Patent No. 6451604
                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
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75.0%;
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Best Local Similarity 75.v.
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Matches 7; Conservative
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GENERAL INFORMATION:
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LENGTH: 247
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-17
STORMER OF SEQ ID NOS: 33142
SEQ ID NO 29670
LENGTH: 369
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Sequence 2, Application US/09120817

Patent No. 6172184

GENERAL INFORMATION:
APPLICANT: Charkowski, Amy
APPLICANT: Alfano, James R.
TITLE OF INVENTION: PSEUDOMONAS SYRINGAE AND ITS USE
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                            Score 35; DB 4; Length 369;
Pred. No. 2.2e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 14603
ZIP: 14603
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: P.O. Box 1051, Clinton Square
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,107
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REPERENCE/DOCKET NUMBER: 19603/1741
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID.NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               66.0%;
85.7%;
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66.7%;
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TYPE: amino acid
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Best Local Similarity 85...
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 PRTTGGG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                2 PRVTGGG 8
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: U.S.A.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                     US-09-252-991A-29670
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252, 991A
PRIOR APPLICATION NUMBER: US 60/74,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
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    Gaps
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                                                                                                                                                                       Sequence 14, Application US/09431614
Facent No. 6624139
GENERAL INFORMATION:
APPLICANT: Mei, Zhong-Min
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
TITLE OF INVENTION: RESISTANCE
TITLE OF INVENTION RESISTANCE
FILE REPERRENCE: 21829/41 (BBC-003)
CURRENT FILING DATE: 1999-11-02
RARLIER PILING DATE: 1998-11-05
NUMBER OF SEQ ID NOSE: 18
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    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
  7,
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Pred. No. 2.5e+02;
1; Mismatches 2,
  1; Mismatches
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PROR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DAIE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 27
US-09-252-991A-27068
; Sequence 27068, Application US/09252991A
; Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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6; Conservative
                                                                               169 TPTATGGGS 177
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                                       1 TPRVTGGGA 9
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US-09-252-991A-24671
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US-09-431-614-14
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Matches
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RESULT 24
US-09-252-991A-29670
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LENGTH: 799
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Fatent No. 6551795
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
ATTLE OF INVENTION: ALGORITICS ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 33082
LENGTH: 460
            APPLICAT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRGIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
SEQ ID NO 27680
LENGTH: 289
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                                                                                                                                                                                                                                                                                                                                                                                                                 69.8%; Score 37; DB 4; Length 289;
87.5%; Pred. No. 81;
Live 0; Mismatches 1; Indels
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5370 Manhattan Circle
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Patent No. 6107060
GENERAL INFORMATION:
APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 87.5
Matches 7; Conservative
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Matches 6; Conservative
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ADDRESSEE: Greenlee,
STREET: 5370 Manhatta
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GENERAL INFORMATION:
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STATE:
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Gaps
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85.7%; Pred. No. 3.1e+02;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.9%; Score 36; DB 3; Length 799; 85.7%; Pred. No. 3.1e+02; cive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sewalt, vincent J. H. APPLICANT: Sewalt, vincent J. H. APPLICANT: Singletary, George W. TITLE OF INVENTION: Production of Modified Polysaccarides FILE REPERENCE: 35.18/206348
CURRENT APPLICATION NUMBER: US/09/731,166
PRIOR PILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
PRIOR PILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28 547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
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                                                  COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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Sequence 12, Application US/09731166
Patent No. 6639126
GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (303) 499-8089 INPORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 799 amino acid TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85...
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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Pred. No. 29;

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Conservative
    Best Local Similarity
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LENGTH: 125
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Matches
                      Matches
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US-09-230-421-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC OTHER INFORMATION: SEQUENCE
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                                                                                                                                                                                               73.6%; Score 39; DB 2; Length 447; 77.8%; Pred. No. 58;
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                                                                                                                                                                                                                                                                                                                                                                                       US-09-230-421-13

US-09-230-421-13

Sequence 13, Application US/09230421

Patent No. 6200577

GENERAL INFORMATION:

APPLICANT: Medical Research Council

TITLE OF INVENTION: THERPESVIRAL ALENTS AND ASSAYS

TITLE OF INVENTION: THERPESVIRAL ALENTS AND ASSAYS

TITLE OF INVENTION: THERPESVIRAL ALENTS AND ASSAYS

TILE REFERENCE: P18189C

CURRENT APPLICATION UNBER: US/09/230,421

CURRENT FILING DATE: 1999-01-25

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FASTESEQ for Windows Version 3.0

SEQ ID NO 13

LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.7%; Score 38; DB 3; Length 19; 100.0%; Pred. No. 4.3; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                        1; Indels
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TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: P181189C
CURRENT APPLICATION NUMBER: US/09/230,421
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID MOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3, Application US/09230421; Patent No. 6200577; GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
            TELEPHONE: (301) 258-5200 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                          : 447 amino acids
amino acid
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Best Local Similarity 100.0
                                                                                                                                                                                                               Local Similarity 77.8
                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                 332 PRVPGGGAL 340
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                                                                                                                  linear
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13 TPRVTGG 19
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SEQ ID NO 3
LENGTH: 144
                                                                                                                                                       US-08-468-857-2
                                                                              LENGIH:
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVERMION: AERGIGNOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 22154
LENGTH: 455
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APPLICANT: LYAIN DOUGETEE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 025796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
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                                      Indels
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; Sequence 22154, Application US/09252991A; Patent No. 6551795
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PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
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; Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 77.0.
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les 6, Conservative
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                                                                                                                       138 TPRVTGG 144
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| PRIIGGGGM 9
                                                                            1 TPRVTGG 7
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REFERENCE/DOCKET NUMBER
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STATE: Maryland
COUNTRY: U.S.A.
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US-08-468-857-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08468852
Patent No. 5792644
GENERAL INFORMATION:
APPLICANT: van den BOCGART, Paul
APPLICANT: VERWEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARZO No. 5792644el Patent Department
                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,852
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,357
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
ADDRESSEE: Biotechnology Research Institute
STREET: 1330-A Piccard Drive
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
APPLICATION NUMBER: EP 91.201.523.7
FILING DATE: 18-Jun-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/904,075
                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: William M. Blacketone
REGISTRATION NUMBER: 29,772
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1300 Piccard Drive
CITY: Rockville
STATE: Maryland
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 447 amino acids
amino acid
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MOLECULE TYPE: protein
US-08-310-357-2
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                                                             STATE: Maryland COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                         20850
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APPLICATION NUMBER: US 08/102,865
PRIOR PADLATON NUMBER: US 07/604,075
PRIOR PADLICATION NUMBER: US 07/604,075
PRIOR APPLICATION NUMBER: US 07/604,075
PROPER CHARACTERISTICS
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RESULT 12
US-08-468-855-2
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                                                                                                                      Query Match

90.6%; Score 48; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DEAD DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,653
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US 08/310,357
PRICA APPLICATION NUMBER: US 08/310,357
PRICATION NUMBER: US 08/310,357
PRILING DATE: 06-AUG-1994
PRICATION NUMBER: US 08/102,865
PRILING DATE: 06-AUG-1993
PRICA APPLICATION DATA:
APPLICATION D
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ADDRESSEE: Akzo No. 5670362el Patent Department
STREET: 1300 Piccard Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: van den BOOGAART, Paul
APPLICANT: Von den BOOGAART, Paul
APPLICANT: KOK, Jacobus Johannus
APPLICANT: VERMEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
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APPLICATION NUMBER:
FILING ADATE: 18-Jun-1991
ATTORNEY/AGENT INFORMATION:
; OTHER INFORMATION: Xaa = L, F or M US-09-692-170C-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08468853
Patent No. 5670362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mary E. Gormley
REGISTRATION NUMBER: 34,409
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258 - 5200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
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US-08-468-853-2
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                                                                                                                                                                                                                       ADDRESSEE: Akzo No. 5780289el Patent Department
STREET: 1300 Piccard Drive
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                              COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,855
FILIAGO DATE: 06-JUN-1995
CLASSIFICATION: 435
Sequence 2, Application US/08468855
Patent No. 5780289
GENERAL INFORMATION:
APPLICANT: van den BOOGAART, Paul
APPLICANT: VOR Jacobus Johannus
APPLICANT: VERMEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: van den BOOGAART, Paul

APPLICANT: KOK, Jacobus Johannus

APPLICANT: VERWGUER, Arnoldus Nicolaus

TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE

NUMBER OF SEQUENCES: 10

CORRESSENDENCE ADDRESS:

ADDRESSEE: Organon Teknika Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,357
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,865
FILING DATE: 06-A0(6-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/604,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/604,075
FILING DATE: 18-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91.201.523.7
FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (301) 258-5200 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 77.8
Matches 7; Conservative
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US-08-310-357-2
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Sequence 8, Application US/09075257A

Patent No. 6074645

GENERAL INFORMATION:
APPLICANT: VORK, JOANNE
TITLE OF INVENTION: OF HUMAN CYTOMEGALOVIRUS
TITLE OF INVENTION: OF HUMAN CYTOMEGALOVIRUS
CORRESPONDENCES: 20
CORRESPONDENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: BART G. NEWLAND
STREET: 555 13TH STREET, NW SUITE 701E
CITT: WASHINGTON
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100.0%; Pred. No. 0.054;
tive 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/075,257A
FILING DATE: 11-MAY-1998
CLASSIFICATION TATA:

FILING DATE: 11-MAY-1998
FILING DATE: 10-FEB-1998
FILING DATE: 10-FEB-1998
FILING DATE: 10-FEB-1998
FILING DATE: 10-FEB-1998
FILING DATE: 10-FEB-1997
FILING DATE: 14-OCT-1997
PRIOR APPLICATION NUMBER: US 08/950,064
FILING DATE: 12-NOV-1996
ATTONNEY/AGENT INFORMATION:
NAME: NEWLAND, BART G
REGISTRATION NUMBER: 31,282
REGISTRATION NUMBER: 31,282
REGISTRATION NUMBER: 31,282
REGISTRATION NUMBER: 31,282
REGISTRATION INFORMATION:
TELEBOMMUNICATION INFORMA
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; OTHER INFORMATION: /note= "Xaa = Leu, Phe, or Met"
US-09-075-257A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. w..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMDTURN: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
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Best Local Similarity 100.0
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FRAGMENT TYPE: internal
                                                                   163 PRVTGGGAM 172
1 TPRVTGGGAM 10
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Sequence 8, Application US/09692170C

Fatent No. 6562345
GENERAL INFORMATION:
FRIENERAL: INFORMATION:
FILE REPRENCE: 1954-346
CURRENT APPLICATION NUMBER: US/09/692,170C
CURRENT APPLICATION NUMBER: US/09/692,170C
CURRENT APPLICATION NUMBER: US 09/534,639
FRIOR APPLICATION NUMBER: US 09/534,639
FRIOR APPLICATION NUMBER: US 09/075,257
FRIOR RILING DATE: 1998-05-11
FRIOR FILING DATE: 1998-05-11
FRIOR FILING DATE: 1998-05-11
FRIOR FILING DATE: 1998-02-10
FRIOR PRILING DATE: 1998-02-10
FRIOR FILING DATE: 1998-02-10
FRIOR FILING DATE: 1998-02-10
FRIOR FILING DATE: 1998-02-10
FRIOR FILING DATE: 1996-02-10
FRIOR FILING DATE: 1996-02-10
FRIOR FILING DATE: 1996-01-12
FRIOR FILING DATE: 1996-01-12
FRIOR FILING DATE: 1996-11-12
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Sequence 8, Application US/09534639
Batent No. 6251399
GENERAL INFORMATION:
APPLICANT: Diamond, Don J
APPLICANT: YORK, JOANNE
TITLE OF INVENTION: CYTOMEGALOVIRUS
TITLE OF INVENTION: CYTOMEGALOVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Human OTHER INFORMATION: Cytomegalovirus Epitope Variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
90.6%; Score 48; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                       FILE REFERENCE: 1954-343
CURRENT APPLICATION NUMBER: US/09/534,639
CURRENT FILING DATE: 2000-03-27
EARLIER APPLICATION NUMBER: 09/075,257
EARLIER APPLICATION NUMBER: 09/01,298
EARLIER FILING DATE: 1998-05-11
EARLIER FILING DATE: 1998-02-10
EARLIER FILING DATE: 1998-02-10
EARLIER FILING DATE: 1997-10-14
EARLIER APPLICATION NUMBER: 08/950,064
EARLIER FILING DATE: 1996-11-12
NUMBER: OF SEQ ID NOS: 20
SEQ ID NO 8
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa = Leu, Phe or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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NAME/KEY: MISC_FEATURE
LOCATION: (10)...(10)
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US-09-692-170C-8
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US-09-534-639-8

RESULT 9

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                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREABLIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,699
FILING DATE: 19-Jan-1999
FILING DATE: 19-Jan-1999
FILING DATE: 23-APPL-1996
ATTORNEY/AGENT INFORMATION:
NAME: KOATOFF, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCY DOCKET NUMBER: 33,980
REFERENCY DOCKET NUMBER: 33,980
TELEPHONE: 215-540-9200
                       ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 53; DB 4; Length 579; Best Local Similarity 100.0%; Pred. No. 0.38;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,699
FILING DATE: 19-Jan-1999
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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Berencsi, Klara
Kari, Csaba
                                                                                               STATE: Pennsylvania
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                                                                           Spring House
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CORRESPONDENCE ADDRESS:
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ZIP: 19477
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100.0%; Score 53; DB 1; Length 631;

Best Local Similarity 100.0%; Pred. No. 0.41;

Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bruggeman, Catharina A.
APPLICANT: Vink, Cornelis
APPLICANT: Namon, Albert
APPLICANT: Stals, Frans
TITLE OF INVENTION: A HUMAN CYTOMEGALOVIRUS COMBINED
TITLE OF INVENTION: ANTIGEN AND ITS USE
                  FILLING DATE: 23-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: KOGNOFÉ, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: 33,980
REFERENCE/DOCKET NUMBER: 33,980
REFERENCE/DOCKET NUMBER: 33,080
REFERENCE/DOCKET NUM
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APPLICATION NUMBER: US 60/015,717
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ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Valeta Gregg
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 07532/003001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,541B
FILING DATE: February 22, 1996
CLASSIFICATION: 435
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TELEPHONE: (415) 322-5070
TELEPAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 631 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.(
Matches 10; Conservative
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MOLECULE TYPE: peptide
US-08-605-541B-12
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Gaps

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Kari, Csaba
TITLE OF INVENTION: No. 6448389el Cytomegalovirus DNA Constructs and
Uses Therefor
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100.0%; Score 53; DB 4; Length 561;

Best Local Similarity 100.0%; Pred. No. 0.37;

Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Micolette, Charles A.
TITLE OF INVENTION: THERAPEUTIC ANTI-CYTOMEGALOVIRUS
TITLE OF INVENTION: COMPOUNDS
FILE REFERENCE: GZ 209500
CURRENT APPLICATION NUMBER: US/09/812,079A
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/191,050
PRIOR APPLICATION NUMBER: 60/191,050
PRIOR APPLICATION NUMBER: 60/254,989
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
       CURRENT APPLICATION NUMBER: US/09/692,170C
                  CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 09/534,639
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 1998-05-11
PRIOR APPLICATION NUMBER: US 09/021,298
PRIOR APPLICATION NUMBER: US 09/021,298
PRIOR FILING DATE: 1997-10-14
PRIOR FILING DATE: 1997-10-14
PRIOR FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09812079A Patent No. 6579970
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Patent No. 6448389
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human cytomegalovirus
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Berencsi, Klara
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Best Local Similarity 100.00
Thes 10; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 561
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Patent No. 6562346
GENERAL INFORMATION:
APPLICANT: Diamond, Don J.
TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS
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APPLICANT: Diamond, Don J
APPLICANT: Diamond, Don J
APPLICANT: Diamond, Don J
APPLICANT: DIAMOND, CYTOMEGALOVIRUS
TITLE OF INVENTION: CYTOMEGALOVIRUS
FILE REFERENCE: 1954-43
CURRENT APPLICATION NUMBER: 09/075,257
EARLIER APPLICATION NUMBER: 09/075,257
EARLIER APPLICATION NUMBER: 09/021,298
EARLIER FILLING DATE: 1998-02-10
EARLIER FILLING DATE: 1998-02-10
EARLIER FILLING DATE: 1998-02-10
EARLIER FILLING DATE: 1997-10-14
EARLIER FILLING DATE: 1997-10-14
EARLIER FILLING DATE: 1997-10-14
EARLIER FILLING DATE: 1997-10-14
EARLIER FILLING DATE: 1997-11-12
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                                                             NAME: NEWLAND, BART G
REGISTRATION NUMBER: 31,282
REFERENCE/DOCKET NUMBER: 1954-112CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
APPLICATION NUMBER: US 08/747,488 FILING DATE: 12-NOV-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09534639
Patent No. 6251399
                                                                                                                                                                       INFORMATION FOR SEG ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 10 anino acids TYPE: amino acid STRANDEDNES: not relevant
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US-09-534-639-7
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FRAGMENT TYPE: internal
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March 7, 2004, 13:02:32; Search time 23 Seconds (without alignments) 22.446 Million cell updates/sec Run on:

US-10-697-055-7 53 Title: Perfect score:

1 TPRVTGGGAM 10 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 389414 segs, 51625971 residues Searched:

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10-SEP-1997 (first entry)

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid modelic acid; (2) a host cell containing the vector; (3) an isolated prolypeptide acid; (2) a nost cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for that has an activity against a biological pathway required for proliferation, or that inhibits or proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, settivity; (11) a culture comprising strains in which the gene or which has a proliferation or the parent or which has a proliferation or the product or which has the remaining the extent or which hash of the strains in which the gene or which has a proliferation or the pane or the product or a gene or which has a proliferation or the product or a gene or which has a proliferation or the pane or th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fits.inpo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proceins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID NO 45835; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Malone C,
Carr GJ,
                                                                                                                                                                                                                                    06-SEP-2001; 2001US-00948993.
25-071-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0072851.
06-MAR-2002; 2002US-0362899P.
                                                                                                                                                 21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                        2001US-00815242
                                                                                                                                                                                                                                                                                                                                                                                     (ELIT-) ELITRA PHARM INC.
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Trawick JD,
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                              WO200277183-A2
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Wall D,
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Sequence 768 AA;

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     Length 768;
                             1; Indels
  67.9%; Score 36; DB 6; I
75.0%; Pred. No. 1.1e+03;
tive 1; Mismatches 1;
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Query Match
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AAW19212 standard; protein; 799 AA. RESULT 50
AAW19212
ID AAW19

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Corn starch branching enzyme IIb (SBEIIb) (AAW19212) is an isoform of starch branching enzyme that shows higher rates of branching with amylopectin rather than amylose as subscrate. A cDNA inser (AAF69229) in plasmid clone pBR240 that expresses SBEIIb has been used as a starting point in the assembly of DNA constructs (see also AAF69730, AAF69736-37) designed to achieve suppression of SBEIIb expression in transgenic corn plants, and thereby to produce novel starches that have properties beneficial in food and industrial applications
                                                                                                        Starch branching enzyme IIb, SBEIIb; corn; maize; antisense; amylopectin; transgenic plant, pBE240.
                                                                                                                                                                                                                                                                                                                                                                                                                      Transgenic corn in which grain derived starch fine structure is controlled - specifically branch chain distribution of amylopectin, useful in preparation of thickened foodstuff.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 50-53; 92pp; English.
                                                                                                                                                                                                                                                                                                            (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                           Hubbard NL, Klein TM, Broglie KE;
                                                                         Corn starch branching enzyme IIb.
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Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

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Gaps

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67.9%; Score 36; DB 2; Length 799; 85.7%; Pred. No. 1.1e+03;

1; Mismatches

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Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticidase, therapeutics and pharmaceutical fruge. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-BABT2017). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bifidobacterium longum NCC2705; Bifidobacterium; bacterial; antidiarrheic; antibacterial; inhibitor of Salmonella; detection; identification; lactic acid bacterium; diarrhoea; pathogenic bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 23649; 21pp + Sequence Listing; English.
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Pred. No. 3.5e+02;
1; Mismatches 2; Indels
                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 23649.
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                              ABB65619 standard; protein; 261 AA.
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                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US009231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 261 AA;
                                                                                                                                                                                                                                         WO200171042-A2
                                                                                                                                                                         pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-NOV-2002
                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                       27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP65988;
                                                              ABB65619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 48
RESULT 47
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             ABB65619
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The present invention describes a polymucleotide (I) comprising a sequence of a Bifidobacterium genome selected from the nucleotide sequences given in ABGB1842 and ABGP1843, or a sequence exhibiting at least 90% identity or which hybridises with the sequence exhibiting at Last 19% identity or which hybridises with the sequence given in ABGB1842 and ABGB1843. Also described is a polymucleotide (II) encoding a cut of the protein comprising a sequence selected from 1097 sequences given in ABGE528 to ABGE6354 ligated in frame to a polymucleotide encoding a cut of the properties, and can be used as an inhibitor of Salmonella. (I) (which is a probe) is useful for the detection and/or identification of Bifidobacterium longum in a biological sample. A carrier containing the sactio acid bacterium Bifidobacterium longum NCC2705 (CNCM I-2618) can be used for preventing and/or treating diarrhoea brought about by pathogenic bacteria and/or rotavirus. The carrier is a food composition selected from tablets, liquid bacterial lased products, milk based fermented products, ince-creams, fermented cereal based products, ince-creams, fermented cereal based products, ince-creams, fermented cereal based products, milk based composition selected from tablets, liquid bacterial suspensions, dried oral supplement, wet cube feeding or wet tube feeding.

(I) is useful in DNA arrays or chips to carry out analysis of the stindard contains gene. ABGE81850 represent or selected.
                                                                                                                                                                                                                                                                                                                                  Novel polynucleotide comprising Bifidobacterium genome sequence useful as a probe or primer for detecting and/or identifying Bifidobacterium longum in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bifidobacterium related nucleotide sequences given in the Sequence Listing from the present invention but not mentioned further within the specification. N.B. The sequence data for this patent is not represented in the printed specification but is based on sequence information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 5; Length 361;
Pred. No. 4.9e+02;
0; Mismatches 1; Indels
rotavirus; food composition; pharmaceutical composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #3438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; SEQ ID NO 732; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU17911 standard; protein; 768 AA.
                                                                                                                                                                   30-JAN-2001; 2001EP-00102050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.9%;
                                                                                                                                                                                                              30-JAN-2001; 2001EP-00102050.
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Best Local Similarity 87.50,
Best Local 7; Conservative
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                                        Bifidobacterium longum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 RCTGGGAM 222
                                                                                                                                                                                                                                                                                                 WPI; 2002-668397/72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 361 AA;
                                                                                EP1227152-A1
                                                                                                                           31-JUL-2002
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Bacillus anthracis.

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1 TPRVTGGG

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74 TPRLNGGG 81

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGK) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). (II) the polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed cartivity of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in the protein protein acceptance in the protein protein and polymucleotide sequences have applications in the protein protein and polymeric diagnostics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fits. Fig. Wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.9%; Score 36; DB 4; Length 98; 75.0%; Pred. No. 1.2e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID NO 32426; 103pp; English.
                                                                                                                                                                                                                                       Novel human diagnostic protein #2058.
                                                                                                        ABG02067 standard; protein; 98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-00540217
                                                                                                                                                                                            (first entry)
96 TPRVFGGG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS66254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                            WO200175067-A2.
                                                                                                                                                                                              13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2001.
                                                                                                                                                     ABG02067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                               RESULT 45
                                                                                      ABG02067
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic matent did not ameas of the invention. Note: The sequence other this partner are the sequence of the nivention. Note: The sequence of the invention but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                         Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 45547; 103pp; English.
                                                                                                                                                   Novel human diagnostic protein #15179.
                                  ABG15188 standard; protein; 146 AA.
                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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Best Local Similarity 77.0.
                                                                                                               18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TPRVTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 TPROTGSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS79375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 146 AA;
                                                                                                                                                                                                                                                                                        WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity.
                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                             11-OCT-2001.
                                                                        ABG15188;
RESULT 46
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0

.. 0

0; Gaps

6; Conservative

Matches

1 TPRVTGGG 8

:||| |||| 53 SPRVHGGGA 61

ABM55760 RESULT

d à

ABM55760 standard; protein; 103 AA.

ABM55760;

(first entry) 20-0CT-2003 Propionibacterium acnes predicted ORF-encoded polypeptide #20436.

Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine

Propionibacterium acnes.

WO2003033515-A1.

24-APR-2003.

11-OCT-2002; 2002WO-US032727.

15-OCT-2001; 2001US-00978825.

(CORI-) CORIXA CORP.

Carter D; Maisonneuve JL; Jones R, Carte Bhatia A, Benson DR, W, Persing DH, S, Lodes MJ, Zhang Y, Wang S, Jen S, Lode Barth B, Vallieve-Douglass J; Skeiky YAW, ng S, Jen S Mitcham JL,

WPI; 2003-381789/36.

N-PSDB; ACF64530.

New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

Example 1; SEQ ID NO 20436; 1481pp; English

The invention relates to an isolated polymucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polymetrides encoded by the polymucleotides (ABMS5624-ABM64536) and to immunogenic fragments of P. acnes polymetrides. The invention additionally encompasses expression vectors and host cells comprising a polymucleotide of the invention, antibodies against polymetrides of the invention, a method for stimulating an immune response specific for a P. acnes polymetride and an isolated T cell population comprising T cells prepared to the invention, a method for stimulating an immune response specific for a P. acnes polymetrides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polymetride); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polymetrides, polymucleotides, antibodies, fusion proteins, proteins T cell populations or antigen-presenting express the proteins T cell populations or antigen-presenting express the express the proteins T cell populations or antigen-presenting express the express the proteins T cell populations or antigen-presenting express the express the expressive proteins are express the expressive presenting or antigen-presenting expressive presenting cells that express the expressive presenting or antigen-presenting expressive presenting or antigen-presenting expressive presenting or antigen-presenting or antigen-presenting or antigen-presenting expressive presenting or antigen-presenting or antigen-presentin and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acres polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present

Sequence 103 AA;

Query Match

69.8%; Score 37; DB 6; Length 103;

. 0 matrix metalloprotease; MWP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glomerulosclerotic renal disease; lung cancer; idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer. antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; Gaps . 1; Indels Human anti-TIMP-1 antibody light chain #26. ed. No. 87; Mismatches Pred. No. ABR'01485 standard; protein; 214 AA. 24-APR-2002; 2002WO-US012801 24-APR-2001; 2001US-0285683P 77.8%; 7; Conservative (FARB) BAYER CORP. (MORP-) MORPHOSYS AG. 53 SPRVHGGGA 61 9 1 TPRVTGGGA Best Local Similarity WO200286085-A2. Homo sapiens. 31-OCT-2002. 16-APR-2003 ABR01485; Matches ABR01485

The invention relates to a novel purified preparation of a human antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1) and neutralises a matrix metalloprotease (MMP) inhibiting activity of TMP and neutralises a variable heavy chain (VHC)DR3 region and a variable light chain (VLC)DR3 region. An antibody preparation of the invention has hepatotropic, cytostatic, nephrotropic and cardiant activity. The human antibody is useful for decreasing an MMP-inhibiting activity of a TIMP-1. It is especially useful for ameliorating the symptoms of a disorder in which TiMP-1 is elevated, e.g. liver fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The antibody is also useful for detecting a TIMP-1 in a test preparation, or in diagnosing a disorder in which a TIMP-1 level is elevated. The sequences shown in ABR01460-ABR01501 represent the light chain regions of a human anti-TIMP-1 antibody of the invention Sequence 214 AA;

New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung

Claim 21; Page 135-136; 228pp; English.

cancer.

Krebs B;

Kraft S,

Hirth-Dietrich C,

Knorr AM, Schauer M,

Pan C,

WPI; 2003-129114/12.

N-PSDB; ABZ74842

0; Gaps ., Length 214; Indels Pred. No. 1.9e+02; Query Match 69.8%; Score 37; DB 6; Best Local Similarity 87.5%; Pred. No. 1.9e+02 Matches 7; Conservative 0; Mismatches

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9908-0155698-
9908-0156458P-
9908-0156596P-
9908-015717P-
9908-0157753P-
9908-0157865P-
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990S-0154779P.
990S-0155139P.
990S-0155486P.
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99US-0158369P.
99US-0159293P.
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99US-0159637P.
99US-0159638P.
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99US-0161361P.
99US-0161920P.
            9903-0148341P.
9903-0148341P.
9903-0148565P.
9903-0148684P.
                                                                                                99US-0149930P.
99US-0150566P.
99US-0150884P.
                                                                                                                       99US-0151065P.
99US-0151066P.
99US-0151080P.
                                                                                                                                             99US-0151303P.
99US-0151438P.
99US-0151930P.
99US-0152363P.
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99US-0153758P.
99US-0154018P.
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99US-0149929P.
99US-0149902P.
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99US-0160741P.
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                                                                                                                                                                                                                                                                                                                             99US-0159329P
                                                                                                                                                                                                                                                                                                                                    99US-0159330P
                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0160815P
                                                    99US-0149175P
                                                            99US-0149426P
                                                                   99US-0149722P
                           13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
18-AUG-1999;
20-AUG-1999;
                                                                                                                                                                           10-SEP-1999;
13-SEP-1999;
15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
23-SEP-1999;
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07-0CT-1999
12-0CT-1999
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21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
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20-AUG-1999;
23-AUG-1999;
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25-AUG-1999;
26-AUG-1999;
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21-0CT-1999)
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21-0CT-1999,
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Query Match
71.7%; Score 38; DB 3; Length 401;
Best Local Similarity 87.5%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypercosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies polypeptides may be used as antigens in the production of antibodies of therefore treat P. acnes proteins. The antibodies and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for the printed in electronic format directly from NIPO at
                                                                                                                                                                                                                                                              SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Persing DH, Mitcham JL, Wang SS, Bhatia A; e J, Zhang Y, Jen S, Carter D;
                                                                                                                                                                                                                            Propionibacterium acnes immunogenic protein #20137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID NO 20436; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                                   AAU59241 standard; protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L'maisonneuve J, Zhang Y,
                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes.
80 TPSVTGGG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS59601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 103 AA;
                                                                                                                                                                                      27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2001.
                                                             RESULT 42
                                                                                AAU59241
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Query Match

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0; Gaps

69.8%; Score 37; DB 4; Length 103; 77.8%; Pred. No. 87; 1; Indels iive 1; Mismatches 1; Indels

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99US-0138640P.
99US-0139464P.
99US-0139451P.
99US-0139451P.
99US-0139451P.
99US-0139451P.
99US-0139456P.
99US-0139456P.
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99US-0139456P.
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9905-0144814P-
9905-0145086P-
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9905-0147388P-
9905-0147388P-
9905-0147388P-
9905-0147388P-
10 - JUN - 1999;
10 - JUN - 1999;
14 - JUN - 1999;
16 - JUN - 1999;
16 - JUN - 1999;
18 - JUN - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUL-1999;
28-JUL-1999;
02-AUG-1999;
02-AUG-1999;
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03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-AUG-1999
                                                                                                                                                               22-JUN-19
23-JUN-19
23-JUN-19
24-JUN-19
28-JUN-1
29-JUN-1
   ·;
                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                    Gaps
                                     .
0
                  Query Match
71.7%; Score 38; DB 3; Length 401;
Best Local Similarity 87.5%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 64199.
                                                                                                                 AAG50642 standard; protein; 401 AA.
                                                                                                                                                                                                                                                                                               990S-0123180P
990S-0123548P
990S-0125788P
990S-0126785P
990S-0126785P
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990S-0128144P
990S-0128045P
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990S-0132484P
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990S-0132487P
990S-0134218P
990S-0134218P
990S-013421P
990S-013562P
990S-013562P
990S-013562P
990S-0136782P
990S-0136782P
    99US-0162142P.
                                                                                                                                                                                                                                                                       25-FEB-2000; 2000EP-00301439
                                                                                                                                                  18-OCT-2000 (first entry)
                                                                                                                                                                                                                     Arabidopsis thaliana.
                                                                       80 TPSVTGGG 87
                                                    1 TPRVTGGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-1999;
21-MAY-1999;
24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
28-MAY-1999;
    PR 29-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
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14-MAY-1999
                                                                                                                                                                                                                                                       06-SEP-2000
                                                                                                                                 AAG50642;
                                                                                                 RESULT 41
                                                                                                           AAG50642
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US-0136392 UUS-0137522 UUS-0137522 UUS-0137522 UUS-0137502 UUS-0137502 UUS-0138440 UUS-0139453 UUS-0139453 UUS-0139453	99US-0139456P. 99US-0139456P. 99US-0139458P. 99US-0139450P. 99US-0139460P. 99US-0139461P. 99US-0139461P. 99US-0139461P. 99US-0139463P. 99US-0139463P. 99US-0139750P. 99US-0139750P. 99US-0139750P. 99US-0140354P. 99US-0140354P. 99US-0140991P. 99US-014154P. 99US-0141280P. 99US-014280P. 99US-014408FP. 99US-014408FP.	902-014339 903-0144339 903-0144339 903-0144884 903-0145086 903-0145089 903-0145089 903-0145089 903-0145089 903-0145192 903-0145218 903-0145218 903-0145218 903-0145218 903-0145218 903-0145218 903-0145218 903-0145318 903-0145318 903-0145318 903-0145318 903-0145318 903-0145318 903-0145318 903-0145318
27 - MAY - 1999; 28 - MAY - 1999; 01 - JUN - 1999; 03 - JUN - 1999; 07 - JUN - 1999; 08 - JUN - 1999; 10 - JUN - 1999; 14 - JUN - 1999; 16 - JUN - 1999; 16 - JUN - 1999; 17 - JUN - 1999; 18 - JUN - 1999; 18 - JUN - 1999;	PR 18-JUN-1999; PR 18-JUN-1999; PR 18-JUN-1999; PR 18-JUN-1999; PR 18-JUN-1999; PR 18-JUN-1999; PR 21-JUN-1999; PR 23-JUN-1999; PR 24-JUN-1999; PR 10-JUL-1999; PR 10-JUL-1999; PR 11-JUL-1999; PR 11-JUL-1999	19-001-1999; 20-001-1999; 20-001-1999; 20-001-1999; 21-001-1999; 21-001-1999; 22-001-1999; 22-001-1999; 22-001-1999; 22-001-1999; 23-001-1999; 23-001-1999; 23-001-1999; 23-001-1999; 27-00

0105 - 0147204P 9US - 0147302P 9US - 0147302P 9US - 0147260P 9US - 0147303P 9US - 0147303P 9US - 0147343P 9US - 0148313P 9US - 0148313P 9US - 0148313P 9US - 0148313P 9US - 0148313P 9US - 0148313P 9US - 0148334P 9US - 0148348P	990S-0149426P. 990S-0149722P. 990S-0149723P. 990S-0149929P. 990S-0149930P. 990S-0149930P. 990S-015066P. 990S-0151066P. 990S-0151066P. 990S-0151066P. 990S-0151066P. 990S-015106P. 990S-015106P. 990S-015108P. 990S-015108P. 990S-015108P. 990S-015108P. 990S-015108P. 990S-015108P. 990S-0154018P. 990S-0154018P. 990S-0154018P. 990S-0154018P. 990S-0154018P.	905-015-596-7905-905-905-905-905-905-905-905-905-905-	903-0160768P 903-0160770P 905-0160814P 905-0160815P 905-0160981P 905-0161404P 905-0161406P 905-0161406P 905-0161406P 905-0161360P 905-0161950P 905-0161950P
04-AUG-1999 04-AUG-1999 05-AUG-1999 05-AUG-1999 06-AUG-1999 09-AUG-1999 11-AUG-1999 12-AUG-1999 13-AUG-1999 13-AUG-1999 13-AUG-1999 13-AUG-1999 13-AUG-1999	PR 18-AUG-1999; PR 20-AUG-1999; PR 20-AUG-1999; PR 23-AUG-1999; PR 23-AUG-1999; PR 25-AUG-1999; PR 25-AUG-1999; PR 27-AUG-1999; PR 21-SEP-1999; PR 11-SEP-1999; PR 11-SEP-1999; PR 12-SEP-1999; PR 12-SEP-1999; PR 22-SEP-1999; PR 23-SEP-1999; PR 23-SEP-1999; PR 24-SEP-1999; PR 24-SEP-1999	24 - 0.58 p. 1.1999 05 - 0.07 - 1.1999 06 - 0.07 - 1.1999 07 - 0.07 - 1.1999 13 - 0.07 - 1.1999 13 - 0.07 - 1.1999 14 - 0.07 - 1.1999 14 - 0.07 - 1.1999 16 - 0.07 - 1.1999 18 - 0.07 - 1.1999 21 - 0.07 - 1.1999	21-0CT-1999 21-0CT-1999 21-0CT-1999 22-0CT-1999 22-0CT-1999 25-0CT-1999 25-0CT-1999 26-0CT-1999 26-0CT-1999 28-0CT-1999 28-0CT-1999

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and the anti-CCP antibody are useful in agriculture to modulate the protein levels or activity of a protein involved in the cell cycle due to derviscommental conditions, including ablotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or bictic stress such as pathogen attack, to modulate e.g. enhance crop yields, and attenuate plant architecture, plant quality traits, plant reproduction and seed development, endoreduplication in storage cells, storage tissues and/or storage organs of plants or its parts. CCP is useful as an immunogen to generate antibodies. CCP protein is useful to screen for naturally cocurring CCP substrates. The polynuclectide is useful for expressing CCP protein, to detect CCP mRNN, or a genetic lesion in a CCP gene and to modulate CCP activity. The present sequence represents a CCP protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription factor polynucleotides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant,
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription factor; transgenic plant; growth rate; senescence; seed germination rate; plant vigor; seedling vigor.
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                                                                                                                                                                                                                                                                                            Score 38; DB 5; Length 383;
Pred. No. 2.3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adam LJ, Dubell An
r TL, Creelman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant yield-related protein from clone G2373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 461; 454pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD30432 standard; protein; 383 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reuber TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MEND-) MENDEL BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-NOV-2001; 2001US-0336049P.
11-DEC-2001; 2001US-0338692P.
                                                                                                                                                                                                                                                                                            71.7%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUN-2002; 2002US-00171468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2002; 2002WO-US025805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001; 2001US-0310847P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Riechmann JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 87.5.
The Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jiang C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                          62 TPSVTGGG 69
                                                                                                                                                                                                                                                                                                                                                                    1 TPRVTGGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-248221/
N-PSDB; ADD30431.
                                                                                                                                                                                                                                                              Sequence 383 AA;
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Pilgrim ML, J
Broun PE;
                                                                                                                                                                                                                          the invention
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such as an alteration in a plant growth characteristic, e.g. growth rate,
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        germination rate of seeds, vigor of plants and seedlings, or leaf and flower senescence. Sequence information related to the polymucleotides and also be used in boinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the proteins of the invention.
                                                                                                                           Gaps
                                                                                                                          0;
                                                                                                  71.7%; Score 38; DB 7; Length 383; 87.5%; Pred. No. 2.3e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 13672.
                                                                                                                                                                                                                                AAG13980 standard; protein; 401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0126785P.
99US-0127462P.
99US-0128234P.
99US-0129845P.
99US-0129845P.
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99US-0132048P.
99US-0132407P.
99US-0132484P.
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99US-0132486P.
99US-0132487P.
99US-0132863P.
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99US-0125788P.
99US-0126264P.
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99US-0134218P.
99US-0134219P.
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99US-0135353P.
99US-0135629P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0136021P
                                                                                                                                                                                                                                                                             17-OCT-2000 (first entry)
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                   termination sequence
                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                        Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                        62 TPSVIGGG 69
                                                                                                                                                  1 TPRVTGGG 8
                                                                              Sequence 383 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-1999;
30-APR-1999;
04-MAY-1999;
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01-APR-1999;
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19-APR-1999;
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06-MAY-1999;
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99US-0147038F.
99US-0147204P.
99US-0147192P.
99US-0147192P.
99US-0147303P.
99US-0147416P.
99US-0147416P.
99US-014793F.
99US-014793F.
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99US-0149902P.
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99US-0150866P.
99US-0150884P.
99US-0151065P.
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99US-0154039P.
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The invention relates to a novel cell cycle protein (CCP) and the polynucleotides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and an anti-CCP antibody is useful for detecting the presence of CCP in a sample. A CCP antibody is useful for modulating the cell cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CCP nucleic acid and polypeptide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat cisorders characterised by insufficient or excessive production of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CCP protein forms which have decreased or collypeptide are useful for modifying cell face, plant development, compounds that plants, initiation, seed set, seed size, seed development, tuber, fruit, leaf formation, shoot and root initiation and/or development, noters: CCP, the polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell cycle protein; CCP; cell cycle regulation; herbicide; plant growth regulator; plant development; abiotic stress; biotic stress; nutrient deprivation; pathogen attack; crop yield; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators.
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                                                                                                                                     71.7%; Score 38; DB 3; Length 383; 87.5%; Pred. No. 2.3e+02; rive 0; Mismatches 1; Indels
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99US-0123548P.
99US-0125548P.
99US-0126788P.
99US-0126785P.
99US-0126785P.
99US-0126785P.
99US-0128234P.
99US-012845P.
99US-0130449P.
99US-0130449P.
99US-0131449P.
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99US-0132484P.
99US-0132484P.
99US-0159584P.
99US-0160741P.
99US-0160767P.
99US-0160768P.
99US-016070P.
99US-016081AP.
99US-016081BP.
99US-0160881P.
99US-0161404P.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
20-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
115-APR-1999;
21-APR-1999;
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30-APR-1999;
30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
  18-OCT-1999;
21-OCT-1999;
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23-APR-1999;
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                                                                                                                                                                                                                                         0; Mismatches
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99US-012316DP.
99US-012548P.
99US-012624P.
99US-012678B5P.
99US-012678FP.
99US-0128214P.
99US-0128214P.
99US-0128214P.
99US-013845P.
99US-013047P.
99US-013049P.
99US-0159294P.
99US-015929FP.
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99US-016081P.
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99US-016081P.
99US-016193P.
99US-0161359P.
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87.5%;
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13-0CT-1999;

13-0CT-1999;

14-0CT-1999;

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05-MAR-1999;
03-MAR-1999;
23-WAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
19-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
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Matches
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9905-0132484P

9905-0132484P

9905-0132484P

9905-0132486P

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9905-0132486P

9905-0134218P

9905-0134218P

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9905-0139452P

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99US-0144331P-
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99US-0143542P.
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99US-0128234P. 99US-0128234P. 99US-0129045P. 99US-0130049P. 99US-013049P. 99US-013089IP. 99US-0131849P. 99US-0131849P. 99US-0131848P. 99US-013248P. 99US-013248P. 99US-013248P. 99US-013248P. 99US-013248P. 99US-013248P. 99US-013248P. 99US-013248P. 99US-013421P. 99US-013421P. 99US-013421P. 99US-013421P. 99US-013421P. 99US-013421P. 99US-013421P. 99US-013422P. 99US-013562P. 99US-013622P. 99US-013648P. 99US-013648P. 99US-013744P. 99US-013744P. 99US-013744P. 99US-013744P. 99US-013744P. 99US-013744P. 99US-013744P. 99US-013744P. 99US-013445P. 99US-013445P. 99US-013945P.	103-0139899) 103-01403531 103-01403531 103-01400595 103-01400991 103-0141084 103-01421084 103-0142085 103-0142085 103-0142085 103-0142085 103-0142085 103-0143624 103-0143624 103-0143624 103-0143624 103-0143624 103-0143624 103-0143624 103-01444086 103-01444086 103-014441086 103-014441086 103-014441086 103-014441086 103-014441086 103-014441086 103-014441086 103-014441086 103-014441086 103-014441086 103-014441086 103-014441086
PR 06-APR-1999; PR 16-APR-1999; PR 16-APR-1999; PR 21-APR-1999; PR 21-APR-1999; PR 23-APR-1999; PR 23-APR-1999; PR 23-APR-1999; PR 23-APR-1999; PR 30-APR-1999; PR 30-APR-1999; PR 06-MAY-1999; PR 10-MAY-1999; PR 14-MAY-1999; PR 16-UN-1999; PR 16-UN-1999; PR 16-UN-1999; PR 16-UN-1999; PR 18-UN-1999; PR 18-UN-	22~JUN-1999; 23~JUN-1999; 24~JUN-1999; 24~JUN-1999; 28~JUN-1999; 30~JUN-1999; 01~JUL-1999; 01~JUL-1999; 06~JUL-1999; 06~JUL-1999; 12~JUL-1999; 13~JUL-1999; 14~JUL-1999; 16~JUL-1999; 16~JUL-1999; 16~JUL-1999; 16~JUL-1999; 16~JUL-1999; 16~JUL-1999; 16~JUL-1999; 16~JUL-1999; 16~JUL-1999; 16~JUL-1999;

US-0144332P US-0144333P US-0144332P US-0144352P US-0144862P US-0144864P US-0145086P US-0145086P US-0145086P US-0145086P US-014508P US-014508P US-014508P	US-0145145F US-0145145F US-0145246F US-0145276F US-0145918P US-0145918P US-0145918P US-0145918P US-0147038F US-0147038F US-0147038F US-014704F US-0147304F US-0147304F US-0147304F US-0147304F US-0147304F US-0147304F US-0147416F	US-014 135 14 15 15 15 15 15 16 16 16 16 16 16 16 16 16 16 16 16 16	990S-0151303P 990S-0151303P 990S-0152363P 990S-0153070P 990S-0153070P 990S-0154018P 990S-0154018P 990S-015402P 990S-0155139P 990S-0155139P 990S-0155139P 990S-015513P 990S-015669P 990S-015669P 990S-015669P 990S-015669P 990S-015669P 990S-015669P 990S-01569P 990S-01569P 990S-0159P 990S-0159P
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cancer; cell proliferative disorder; autoimmune disorder;
hillammalory disorder; infection; hormonal disorder; metabolic disorder;
neurological disorder; gastrointestinal disorder; transport disorder;
connective tissue disorder; drug screening; proteome analysis;
gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
disease model; toxicological testing; transcript imaging;
intracellular signalling.
involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                    Length 197;
                                                                                                                                                                                                          DB ...
                                                                                                                                                                                                      71.7%; Score 38; DB 4;
85.7%; Pred. No. 1.2e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human DITHP intracellular signalling protein.
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29-MAR-2001; 2001US-0280068P.
16-MAY-2001; 2001US-0291280P.
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17-MAY-2001; 2001US-0291849P.
19-UUN-2001; 2001US-0299428P.
20-UUN-2001; 2001US-0299776P.
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Matches 6; Conserv
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The invention relates to novel human diagnostic and therapeutic

polymucleotides designated dithp (ACC46080-ACC46749) and to their encoded

polymucleotide sequences at least 90% identical to the dithp cDNA

comparison (DITHP) ABRA1136-ABRA1812). The invention also relates to

polymucleotide sequences at least 90% identical to the dithp cDNA

comparison of DITHP proteins, not cells and

crecombinant production of DITHP proteins; antibodies specific for DITHP

proteins microarrays comprising dithp nucleic acid sequences; methods of

corceins microarrays comprising the nucleic acid sequences; methods of

corceins dithp nucleotide and protein sequences; methods of

casessing the toxicity of test compounds using a dithp hybridisation

corpose. Dithp nucleic acid sequences and DITHP proteins may be used in the

diagnosis of a wide variety of conditions including cancer and other cell

corposes of a wide variety of conditions including cancer and other cell

corposes of a wide variety of conditions including cancers; metabolic

corposes of a wide variety of conditions including cancer and other cell

corposes of a wide variety of conditions including cancer in the connective tissue disorders; metabolic

disorders; neurological disorders; gastrointestinal disorders; transport

corposes and connective tissue disorders. They may also be used to

sorceen for modulators of protein acitivity or gene expression. DITHP

corposeders and to induce antibodies. The dithp nucleic acids are

additionally useful in somatic or germline gene therapy of the disorders in

corposeders and to induce antibodies. The dithp nucleic acids are

controlled above, as a source of antisense sequences, as a source of

the general or protein and additionally and identification of individuals, in

the formal of the protein and the protein and the disorders in the connection and and the protein of the protein and the protein of the protein of the protein of the protein of the p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                  Claim 27; SEQ ID NO 804; 591pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 TPRVTGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TPRVTGG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1033405-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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01-APR-1999;

Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies.

Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J; , Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR; SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH; H, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;

Dufour GE, Hillman JL, Daughtery SC, Dam TC,

Daffo A,

Peralta CH,

Flores V,

Lan RY, Urashka ME;

го В

Marwaha R,

WPI; 2003-129518/12.

N-PSDB; ACC46211.

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RESULT 32
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                                                                                                                                          The present sequence is a herpes simplex virus (HSV) truncated tegument protein VP22 derived peptide. VP22 was used in the preparation of a novel mativital agent, which inhibits the maturation and/or replication of HSV by disrupting association between VP22 and VP16 and/or gB. The agent can be used to treat, e.g. cold sores, genital herpes, chickenpox and
                                                                                                                                                                                                                                                                                                                                                                      HSV; tegument protein; VP22; UL49; antiviral agent; treatment; cold sore;
                                                                                             New antiviral agent disrupting binding of VP22 to VP16 or gB - useful for treating infections caused by herpes simplex, e.g. cold sores and chicken
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                   71.7%; Score 38; DB 2; Length 19; 100.0%; Pred. No. 9.8;
                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                         Herpes simplex virus truncated tegument protein VP22
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "residues 158-267 of VP22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rixon HWM;
                                                               Rixon HWM
                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "histidine tag motif"
                                                                                                                                                                                                                        100.0%; Prea. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                               132. .144
/note= "epitope tag motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hope RG,
                                                                                                                                                                                                                                                                                                                                                                                genital herpes; chickenpox; shingles
                                                              Hope RG,
                                                                                                                                                                                                                                                                                                                                                                                                                        cocation/Qualifiers
                                                                                                                                                                                                                                                                                                           AAW47195 standard; peptide; 144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                Herpes simplex virus unknown type.
                                                                                                                               Example; Page 25; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-GB002036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96GB-00015726
                97WO-GB002036.
                                96GB-00015726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MEDI-) MEDICAL RES COUNCIL.
                                                (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcgeoch DJ,
                                                                Mclaughlan J, Mcgeoch DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                22. .131
/note= "r
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-130696/12.
                                                                                WPI; 1998-130696/12.
                                                                                                                                                                                                                                                                   13 TPRVTGG 19
                                                                                                                                                                                                                            Local Similarity
hes 7; Conserv
                                                                                                                                                                                                                                                   1 TPRVTGG 7
                                                                                                                                                                                                    Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mclaughlan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9804708-A1
                                                                                                                                                                                                                                                                                                                                         03-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-FEB-1998
                                 26-JUL-1996;
   05-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                           AAW47195;
                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in danostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders
New antiviral agent disrupting binding of VP22 to VP16 or gB - useful for treating infections caused by herpes simplex, e.g. cold sores and chicken
                                                                                                                                                                                               The present sequence is the herpes simplex virus (HSV) truncated tegument
                                                                                                                                                                                                                                                                                             рę
                                                                                                                                                                                                                          protein VP22. VP22 was used in the preparation of a novel antiviral agent, which inhibits the maturation and/or replication of HSV by disrupting association between VP22 and VP16 and/or gB. The agent can be used to treat, e.g. cold sores, genital herpes, chickenpox and shingles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polymucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.7%; Score 38; DB 100.0%; Pred. No. 83; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 47092; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #16724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG16733 standard; protein; 197 AA.
                                                                                                                                         Example; Page 52; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-00540217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-2000; 2000US-00649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 TPRVTGG 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>r</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TPRVTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAS80920
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 144 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-0CT-2001
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X B X S S X X X X X B X B X B X Y X Y X B
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                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a peptide which was used to form a linker between chimaeric proteins consisting partially of the hepatitis C virus core protein. The core protein has been shown to be localised to lipid droplete within cells. This means that fragments of the protein, in particular those comprising amino acids 125-144 or 161-166, can be used to target proteins to lipid droplets in milk. This provides a simple and efficient means of obtaining proteins of interest, using transgenic animals. Proteins of interest include those implicated in disease and antigenic polypeptides for use as vaccines
          ó
                                                                                                                                                                                                                                                                                                                                                    Protein comprising a lipid globule targeting sequence consisting of a heparitis C virus core protein, useful for targeting a protein of interest to lipid globules which are subsequently secreted into animal milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cytomegalovirus strain AD169 pp65 peptide fragment SEQ ID 128.
          ;
                                                                                                                                                                           Hepatitis C; targeted protein production; core protein; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.7%; Score 38; DB 3; Length 10;
Pred. No. 1.8e+02;
L; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                         Chimaeric hepatitis C virus core protein linker peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB86671 standard; peptide; 15 AA.
                                                                                                AAB01253 standard; protein; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                       Example; Page 42; 60pp; English.
                                                                                                                                                                                                                                                                           98GB-00025953.
                                                                                                                                                                                                                                                         99WO-GB003898.
                                                                                                                                                                                                                                                                                              (MEDI-) MEDICAL RES COUNCIL.
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100...
7; Conservative
            Conservative
                                                 332 PRVPGGGAL 340
                                                                                                                                                                                                                                                                                                                  Mclauchlan J;
                             2 PRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                      WPI; 2000-400040/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPRVTGG 10
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 Best Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 AA;
                                                                                                                                                                                                                  WO200031127-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-2001
                                                                                                                                                                                                                                                         23-NOV-1999;
                                                                                                                                                                                                                                                                           26-NOV-1998;
                                                                                                                                      19-DEC-2000
                                                                                                                                                                                                                                      02-JUN-2000
                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB86671;
                                                                                                                   AAB01253;
                                                                                                                                                                                                                                                                                                                 Hope G,
                                                                             RESULT 28
                                                                                        AAB01253
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This sequence represents a novel method for stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and the determination of the response to an antigen (I). The method comprises (i) dividing the amino acid sequence of the antigen into protein fragments (II) of at least 9 amino acids, whereby adjacent or neighbouring fragments are in the whole antigen sequence; (ii) synthesizing a peptide library containing (II); and (III); and (III) in a single culture vessel. The method is used to immunocery expiniting (II) in a single culture vessel. The method is used to immunocery expinitate T cells of mammals, particularly humans, and is also useful for diagnostic purposes to determine if a mammal, especially human, has previously immunologically responded to a specific protein, and to determine strength of that response. The method is suitable for in vivo or in vitro immuno-stimulation of mammalian, more preferably human T lymphocytes, where the stimulated T lymphocytes are expanded and can be transfused into a partient. ARB86614-ARB8603 represent fragments of the human cycomegalovirus IE1 and pp65 lower matrix phosphoprotein which are used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSV; tegument protein; VP22; UL49; antiviral agent; treatment; cold sore; genital herpes; chickenpox; shingles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and the determination of the response to the antigen comprises using a synthetic peptide library of the specific antigen.
Antigen-specific stimulation, T-lymphocyte, CD8 stimulation, pp65; CD4 stimulation; immuno-stimulation; IE1; lower matrix phosphoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSV truncated tegument protein VP22 derived peptide J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reinke P, Faulhaber N, Surel I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW47205 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             simplex virus unknown type.
                                                                                                                                                                                                                                                                                                                                                            17-FEB-2001; 2001WO-EP001773.
                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-2000; 2000DE-01009341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Fig 2; 85pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                        Human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-557718/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPRVTGG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kern F, Volk H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 AA;
                                                                                                                                                                                                   WO200163286-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KERN/) KERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9804708-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-1998
                                                                                                                                                                                                                                                                                 30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW47205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 30
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Gaps

0;

Length 447;

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This sequence represents the Eimeria antigen Eam200. It is useful as a
                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 23; 52pp; English.
                                                                                                                                                                                                                         Bimeria antigen Eam200.
                                                                                                                                                                                                                                                                                                  (ALKU ) AKZO NV.
(ALKU ) AKZO NOBEL NV
                                                                                                                                                         ||:||||:
43 PRITGGGS 50
                                                                                                                                                                                                                                                                                                                           WPI; 1992-425765/52.
                                                                                                                                                   2 PRVTGGGA 9
                                                                                                                                                                                                                                                 Eimeria acervulina.
                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ31997
                                                                                                                      Sequence 339 AA;
                                                                                                                                                                                                                                                                              10-JUN-1992;
                                                                                                                                                                                                                                                                                        18-JUN-1991;
                                                                                                                                                                                                          25-MAR-2003
28-APR-1993
                                                                                                                                                                                                                                                           EP519547-A2
                                                                                                                                                                                                                                                                     23-DEC-1992
                                                                                                                                                                                                AAR29924;
                                                                                                                                          Matches
                                                                                                                                                                                 AAR29924
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vaccine for protecting chickens against coccidiosis. It is also useful an immunoassay reagent. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                  / Match 73.6%; Score 39; DB 2; Length 447 Local Similarity 77.8%; Pred. No. 1.8e+02; nes 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                         AAW58567 standard; protein; 447 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant virus vector.
                                                                                                                                                                                                                                           332 PRVPGGGAL 340
                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ALKU ) AKZO NOBEL NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                      2 PRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1998-232628/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eimeria acervulina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAV31335
                                                                                   Sequence 447 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP838522-A2
                                                                                                                                                                                                                                                                                                                                                                                                                   27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                AAW58567;
                                                                                                                          Query Match
        vaccine
                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                    RESULT 27
                                                                                                                                                                                                                                                                                                                         AAW58567
                                                                                                                                                                                                                                                                                                                                                              8.83333
                                                                                                                                                                                                        ð
                                                                                                                                         a channel activating processes 1 (CAPI is a serine processe and there is no native expression of endogenous CAPI is a serine processe and there is no native expression of endogenous CAPI gene. Transgenic mice which a terrologous disruption in the CAPI gene exhibit an increased susceptibility to seizures which are similar to epilepsy. Disclosed is a method for producing the transgenic mouse with a disruption in the CAPI gene which contains a targeting construct comprising a first or second portion; respectively, of the CAPI gene and a selectable marker. Also disclosed are methods for identifying an agent that modulates susceptibility to esizure or the phenotype, for identifying a potential therapeutic agent correating epilepsy, for evaluating a potential therapeutic agent capable of affecting a condition associated with a mutation in a CAPI gene (e.g. a CAPI agonist) and for determining whether an agent modulates a CAPI serine protease. The transgenic mouse, comprising a disruption in a CAPI gene, is useful for preparing a pharmaceutical composition for treating epilepsy. The sequence presented is the mouse CAPI protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                            The invention discloses a new transgenic mouse comprising a disruption in
                          New transgenic mouse comprising a disruption in a CAP1 gene, useful for preparing a pharmaceutical composition for treating epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eimeria, coccidiosis, chickens, fowl, vaccines, immunise, vaccinate, immunoassay, test, detection, 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.6%; Score 39; DB 6; Length 339; 75.0%; Pred. No. 1.4e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vermeulen AN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New protein-contg. epitope(s) of Eimeri
anticoccidiosis vaccines and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR29924 standard; protein; 447 AA.
                                                                                     Disclosure, Fig 2; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kok JJ, Van Den Boogaart P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92EP-00201673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91EP-00201523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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The Eimeria acervulina 200 kD antigen, recombinant vector viruses or host cells are used to produce vaccines to protect avians against coccidiosis particularly chickens. The vaccine can also contain immunogens related to other pathogens found in poultry or may contain nucleic acid encoding them e.g. antigens of Marek's Disease virus, Newcastle Disease virus, Chicken for Infectious Bronchitis virus, Infectious Bursal Disease virus, Chicken Anaemia Agent, Reo virus, Avian Retro virus, Fowl Adeno virus, Turkey Rhinotrachetits virus, E. Coli or other Eimeria species to produce a multivalent vaccine. The nucleic acids are useful as hybridisation probes to isolate sequences encoding functional variant proteins e.g. from clissues or a cDNA library from a specific Eimeria strain. The nucleic acid is additionally used in test kits for diagnosis of Eimeria Cc infections and infunuoassays. (Updated on 25-WAR-2003 to correct PF field.) (Updated on 25-WAR-2003 to correct PF field.) (Updated on 27-AUG-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New proteins or fragments having immunogenic determinants of Eimeria antigens, nucleic acid, recombinant vector, host cell and antibody - used as vaccine against coccidiosis in avians e.g. chickens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 447;
                                                                                        Eimeria acervulina; vaccine; coccidiosis; poultry; avian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vermeulen AN;
Eimeria acervulina 200kD antigen fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.6%; Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 23-25; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Van Den Boogaart P, Kok JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97EP-00203394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91EP-00201523
92EP-00201673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 447 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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28-NOV-2002.

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ABJ37972 standard; peptide; 9 AA.
                              (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
            07-FEB-2002; 2002WO-IB003040.
                     07-FEB-2001; 2001FR-00001659
                                                                                                                                                                                            Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                         Human cytomegalovirus.
                                                                                                                                                                                                                          84 PRVTGGGA 91
                                                                                                                                                                                                                 2 PRVTGGGA 9
                                                        WPI; 2003-148459/14
                                                                                                                                                                                                                                                                                                                  WO2003000720-A1.
                                                                                                                                                                                       Sequence 172 AA;
                                                                                                                                                                                                                                                                                                 transplantation
                                               Buchrieser C;
                                                                                                                                                                                                                                                                  22-MAY-2003
                                                                                                                                                                                                                                                                                                                           03-JAN-2003.
                                           Duchaud E,
                                                                                                                                                                                                                                            ABJ37972
                                                                                                                                                                                                                                       RESULT
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The invention relates to a novel isolated peptide comprising one or more cytotoxic T-lymphocyte (CTL) epitope(s) of the same or different antigen of a human cytomegalovirus (HCMV). The HCMV antigens can comprise pp28, pp50, pp65, pp71, pp150, gB, gH, IE-1, IE-2, IG2, US2, US3, US6, US11 or UL18. The peptide comprises a sequence of about 9-20 contiguous amino acids of treating cytomegalovirus infection in humans, and in monitoring immune responses in various clinical settings (e.g. transplantation or pregnancy). This sequence represents a human cytomegalovirus CTL epitope peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse, enzyme; transgenic; channel activating protease 1; CAP1; serine protease; seizure; epilepsy; therapeutic; agonist; anticonvulsant.
                                                                                                                                                                                                                                                                                         for diagnosing, preventing or treating CMV infection, comprises pp28, pp50, pp65, pp71, pp150, gB, gH, IE-1, IE-2, US2, US3, US6, US11 or UL18.
                                                                                                                                                                                                                                                                         New human cytomegalovirus (CMV) cytotoxic T-cell epitope peptide, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.4%; Score 41; DB 6; Length 9;
100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse channel activating protease 1 (CAP1) protein.
                                                                                                                       (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                          Walker SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG72018 standard; protein; 339 AA.
                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 105; 308pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAR-2002; 2002WO-US009786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-AUG-2001; 2001US-0311055P.
28-MAR-2002; 2002US-00109616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAR-2001; 2001US-0280509P
                                                                       26-JUN-2001; 2001AU-00005931.
                  26-JUN-2002; 2002WO-AU000829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
Les 8; Conservative
                                                                                                                                                                          Elkington RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 RVTGGGAM 10
                                                                                                                                                                                                                         WPI; 2003-300379/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RVTGGGAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200283875-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Active-site
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                                                                                                                                                                            Khanna R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG72018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG72018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are proteins from Photorhabdus luminescens. The isolated sequences are generated so fprobes and primers for detecting the genome of P. luminescens and related species, to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the colympetides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that can mals or microcorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. combinant production of the proteins, particularly toxins and creaminated to express the genes are useful for recombinant production of the proteins, particularly toxins and creaminated to protein that are sensitive to P. luminescens encoded toxins or antibiotics) and as compensationes. Other uses of the genes and Ab are also useful care sensitive to P. luminescens-encoded toxins or antibiotics) and as compensationes. Other uses of the genes and the proteria are sa virulence factors and for identifying targets of human diseases for which P. C. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virucide; immunostimulant; cytotoxic T-lymphocyte; CTL; epitope; antigen; human cytomegalovirus; HCMV; pp28; pp50; pp65; pp71; pp150; gB; gH; IE-1; IE-2; US2; US3; US6; US11; UL18; cytomegalovirus infection; pregnancy;
                                                                                                                                                                                                                                                                                                                                                                            Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                         Danchin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.1%; Score 43; DB 6; Length 172; 100.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                         Glaser P, Frangeul L, Kunst F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cytomegalovirus CTL epitope peptide SEQ ID No 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Prec. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; SEQ ID NO 2842; 1205pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                         Taourit S,
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(DELT-) DELTAGEN INC

WPI; 2003-058636/05.

N-PSDB; ABS56430

0

0; Gaps

us-10-697-055-7.rag

Virucide; immunostimulant; cytotoxic T-lymphocyte; CTL; epitope; antigen; human cytomegalovirus; HCMV; pp28; pp50; pp65; pp71; pp150; gB; gH; IE-l; IE-1; US2; US3; US6; US11; UL18; cytomegalovirus infection; pregnancy;

Human cytomegalovirus CTL epitope peptide SEQ ID No 8.

22-MAY-2003 (first entry)

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Inducing or sustaining immunological cytotoxic T lymphocyte response in a mammal, useful for treating a mammal with malignant tumor or infectious disease, by directly administering an antigen to the lymphatic system of
                                                                                                                                                             Major histocompatibility complex; MHC; MHC class I molecule; virus; epitope; cytotoxic I lymphocyte response; CTL response; lymphatic system; antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia; lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;
                                                                                                                                                                                                           acquired immune deficiency syndrome; AIDS
                                                                                                                                         MHC class I molecule, viral epitope #148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 22; 73pp; English.
                                                                    ABG79900 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                      (CTLI-) CTL IMMUNOTHERAPIES CORP.
                                                                                                                                                                                                                                                                                                                                02-FEB-2001; 2001US-00776232.
                                                                                                                                                                                                                                                                                                       22-JAN-2002; 2002WO-US002033
                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                            Kundig TM, Simard JJL;
                                                                                                                                                                                                                                    Human cytomegalovirus
WPI; 2002-657506/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 AA;
                                                                                                                                                                                                                                                            WO200262368-A2
                                                                                                                   15-NOV-2002
                                                                                                                                                                                                                                                                                 15-AUG-2002.
                                                                                             ABG79900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                 RESULT 21
                                                             ABG79900
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The invention relates to a method of inducing and/or sustaining an immunological cytotoxic T lymphocyte (CTL) response in a mammal comprising administering directly to the lymphatic system of the mammal:

(a) an antigen in the form of a polypeptide; (b) a vector comprising a nucleic acid encoding the antigen; or (c) a non-peptide antigen. The method is useful for inducing and/or sustaining CTL response in a mammal. This is particularly useful for treating a mammal having a malignant tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious disease (e.g. heptilis, acquired immune deficiency syndrome (AIDS), malaria, measles or tuberculosis), or in an animal having a predisposition to these diseases. The mammal may be dogs, cats, mice, actile, sheep, pigs, goats, rabbits, or preferably humans. ABG79753-ABG80119 represent viral epitopes on major histocompatibility complex (MHC) class I molecules, used in the method of the invention
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Gaps ;

The invention relates to a novel isolated peptide comprising one or more cytotoxic T-lymphocyte (CTL) epitope(s) of the same or different antigen of a human cytomegalovirus (HCMV). The HCMV antigens can comprise pp28, pp50, pp55, pp71, pp150, pg 94, IE-1, IE-1, IE-2, US2, US3, US6, US11 or UL18. The peptide comprises a sequence of about 9-20 contiguous amino acids of the antigen. The peptide epitopes are useful in diagnosing, preventing or treating cytomegalovirus infection in humans, and in monitoring immune responses in various clinical settings (e.g. transplantation or pregnancy). This sequence represents a human cytomegalovirus CTL epitope peptide of the invention

Sequence 11 AA;

New human cytomegalovirus (CMV) cytotoxic T-cell epitope peptide, useful for diagnosing, preventing or treating CMV infection, comprises pp28, pp50, pp65, pp71, pp150, gB, gH, IE-1, IE-2, US2, US3, US6, US11 or UL18.

Claim 105; Page 133; 308pp; English.

(COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

26-JUN-2002; 2002WO-AU000829 26-JUN-2001; 2001AU-00005931

Human cytomegalovirus.

WO2003000720-A1

03-JAN-2003.

transplantation.

Khanna R, Elkington RA, Walker SJ;

WPI; 2003-300379/29.

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Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
83.0%; Score 44; DB 6; Length 11;
100.0%; Pred. No. 0.5;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                        Photorhabdus luminescens protein sequence #2842.
                                                                                                                                                                ABM69745 standard; protein; 172 AA.
                                                                                                                                                                                                                            (first entry)
                               8; Conservative
                                                           1 TPRVTGGG 8
          Best Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                   whooping cough.
                                                                                                                                                                                                                            20-NOV-2003
                                                                                                                                                                                              ABM69745;
   Query Match
                                                                                                                                      RESULT 23
                                                                                                                                                    ABM69745
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Photorhabdus luminescens

WO200294867-A2

ABJ37950 standard; peptide; 11 AA.

RESULT 22 ABJ37950 ID ABJ3 XX

9; Conservative

1 TPRVTGGGAM 10 TPRVTXGGAM 12

Sun Mar

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The invention relates to immunologically active peptides, and functional variants thereof. Capable of eliciting a cellular immune response to dimman cytomegalovirus (HCMV) in humans. The peptides are capable of directing human cytotoxic T lymphocytes (CTL) to recognise and lyse human cells infected with HCMV. Such immunologically active peptides, in molecule, are recognised by CTLs of individuals having a latent (inactive) HCMV infection. Vaccines comprising these peptides are useful for activating CTLs and CTL precursors (CTLp), particularly for eliciting a cellular immune response against HCMV by normal and immunodeficient subjects. The peptides may be used in an assay for determining the degree of immunostimulation caused by HCMV. The peptides may also be used in an assay for determining the degree of immunostimulation caused by HCMV. The peptides may also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        distinguishing individuals who are seropositive from those who have not been exposed to HCMV (seronegative individuals). The present peptide sequence is a cytotoxic epitope variant from human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptides that are immunogenic epitopes of the human cytomegalovirus (CMV), useful for activating cytotoxic T lymphocytes (CTL) or CTL precursors to elicit an immune response against human CMV by normal or immunodeficient subjects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cytomegalovirus, HCMV, cytotoxic epitope, infection, vaccine, cytotoxic T lymphocyte, CTL, CTL precursor; CTLp, Class I antigen, emajor histocompatibility Compis. MHC, cellular immune response; CTL activator; C
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytomegalovirus (HCMV) cytotoxic epitope variant #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.6%; Score 48; DB 4; Length 10; 100.0%; Pred. No. 0.091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Leu, Phe, Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                  AAE05432 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-00747488.
97US-00950064.
98US-00021298.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-00075257.
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-431950/46.
TPRVTGGGA
                                                               TPRVTGGGA
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                                                                                                                                                                                                                                                                                                                                                                         24-SEP-2001
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14-OCT-1997;
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                                                                                                                                                                                                                                                                                                     AAE05432;
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                                                                                                                                                                  RESULT
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The invention relates to immunogenic peptides derived from human cytomegalovirus (HCMV) which are recognised by human cytotoxic T lymphocytes (CTL). The invention also discloses a vaccine against HCMV comprising one of the peptides, and a pharmaceutically acceptable carrier, a cellular vaccine against HCMV comprising antigen presenting cells that have been treated in vitro so that they express the peptide, and a recombinant viral vector vaccine sypressing a gene encoding the peptide. The vaccine is used to modulate the immune response to human cytomegalovirus infection. HCMV is implicated in a number of diseases and conditions including restenosis after coronary angioplasty, morbidity/mortality in AIDS (acquired immunodeficiency syndrome) patients, viral retinitis leading to blindness, encephalitis, enterities, morbidity/mortality in AIDS (acquired immunodeficiency syndrome) patients, viral retinitis leading to blindness, encephalitis, enterities, ascroma) and post-bone marrow transplant complications. The present sequence is an HCMV pp65 based immunogenic epitope peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New immunogenic peptides useful as a vaccination against cytomegalovirus infection, comprises epitopes of human cytomegalovirus which are recognized by human cytotoxic T-lymphocytes.
                                                                                                                                                                                                                                                                                    Immunogenic epitope, pp65; cytotoxic T cell; CTL; HCMV; vaccine; virucide; restenosis; coronary angioplasty; morbidity; mortality; AIDS; acquired immunodeficiency syndrome; viral retinitis; blindness; encephalitis; enteritis; mononucleosis; interstitial pneumonia; malignancy; Karposi's sarcoma; post-bone marrow transplant complication.
                                                                                                                                                                                                                                                   Human cytomegalovirus pp65 protein based immunogenic epitope #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.6%; Score 48; DB 5; Length 10; 100.0%; Pred. No. 0.091; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Leu, Phe, Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                    AAU10827 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Page 10; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAR-2000; 2000US-00534639.
20-OCT-2000; 2000US-00692170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAR-2001; 2001WO-US008576
                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              Human cytomegalovirus
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1 TPRVTGGGA
                                    TPRVTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 10
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                                                                                                                                                                                                                 14-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diamond DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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                                                                                             RESULT 20
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Gaps

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9; Conservative

Best Local Similarity

Query Match Matches 1 TPRVTGGGA 9

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Gaps

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0; Indels

100.0%; Preq. nc.

9; Conservative

Best Local Similarity Matches 9; Conserv

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The present invention describes immunologically active peptides (IAPS) capable of eliciting a cellular immune response to human cytomegalovirus (hCMV). The IAP can be used in a (cellular) vaccine to augment the immune system response to HCMV, or to provide immunity against HCMV. The IAP (cellular) vaccine can also protect an individual having a latent HCMV infection from reactivation. An antigen presenting cell can be used to determine the presence or absence of HCMV-infected Ilymphocytes. The viral vector containing IAP encoding DNA can also be used to provide immunity against HCMV. The IAP can be used to prepare HCMV-reactive human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytocoxic T lymphocytes. The antigen presenting cells primed with the IAPB can be used as diagnostic reagents to detect immunostimulation by HCMV. They can also detect active HCMV infection or exposure to HCMV. HCMV can cause opportunistic infections resulting in a variety of complications in, e.g. immunosuppressed patients. The IAP vaccines impart immunity to bone marrow transplant recipients, solid organ recipients, heart patients, AIDS patients or women of child-bearing years, without the need for ex vivo expansion of HCMV-specific cytocoxic T lymphocytes (which requires sophisticated laboratory setup and is highly labor-
                                                                                                                                                                    Human cytomegalovirus; hCMV; immunologically active peptide; vaccine; immune response; cytotoxic T lymphocyte; CTL; immunostimulation; infection; immunosuppression; bone marrow transplant; solid organ; heart;
                                                                                                                                  Immunogenic peptide cytotoxic I lymphocyte epitope SEQ ID NO:8 of hCMV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic peptide cytotoxic T lymphocyte epitopes of human
                              AAY09315 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 49; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-00950064.
98US-00021298.
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Best Local Similarity 100..
                                                                                                     08-JUL-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CITY ) CITY OF HOPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      York J;
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                                                                                                                                                                                                                                                                    Human herpesvirus 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytomegalovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diamond DJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-1999.
                                                                                                                                                                                                                                                                                       Synthetic
                                                                   AAY09315;
RESULT 17
                   AAY09315
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/label= Leu, Met, Phe Location/Qualifiers

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The present invention describes a cellular vaccine (I), which elicits a MHC Class I cellular immune response to human cytomegalovirus (HCMV), and comprises a peptide selected from (i) - (v), provided that (i) is not concrises a peptide selected from (i) - (v), provided that (i) is not casa (iu) it is not casa (iu) is not case (iu) is not casa (iu) is no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               distinguish individuals who are seropositive from those who have not been exposed to HCMV and in the study of the Class I antigen-processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New immunogenic peptides useful for providing immunity against cytomegalovirus (CMV) infections, are capable of eliciting cellular
                                                                                                                                                                                                                                          Immunogenic; cytotoxic T lymphocytes; CTL; cytomegalovirus; HCMV; infection; immune response; vaccine; immunostimulant; antiviral;
                                                                                                                                                                                          Human cytomegalovirus immunogenic peptide SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                 immunosuppressive; immunity; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Leu, Phe, Met
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                            AAB12413 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-00747488.
97US-00950064.
98US-00021298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune response to human CMV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00075257.
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                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CITY ) CITY OF HOPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-430383/37.
                                                                                                                                                                                                                                                                                                                                                   Human herpesvirus 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 10
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                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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RESULT 18
                          AAB12413
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0;

Gaps

0;

Query Match
90.6%; Score 48; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels

; 0

0; Gaps

90.6%; Score 48; DB 2; Length 10; 100.0%; Pred. No. 0.091; iive 0; Mismatches 0; Indels

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Sequence 631 AA;

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stimulate T cells of mammals, particularly humans, and is also useful for diagnostic purposes to determine if a mammal, especially human, has previously immunologically responded to a specific protein, and to determine strength of that response. The method is suitable for in vivo or in vitro immuno-stimulated mammalian, more preferably human T lymphocytes, where the stimulation of mammalian, more preferably human T ransfused into a patient. AAB86544-AAB86803 represent fragments of the human cytomegalovirus IBI and pp65 lower matrix phosphoprotein which are used to illustrate the method of the invention
            8888888888%
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Sequence 561 AA;

; 0 100.0%; Score 53; DB 4; Length 561; 100.0%; Pred. No. 0.87; ive 0; Mismatches 0; Indels 10; Conservative 1 TPRVTGGGAM 10 Local Similarity Query Match Matchee ò

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Gaps

417 TPRVTGGGAM 426

AAW23036 standard; protein; 631 AA. AAW23036; RESULT 15 AAW23036

Human cytomegalovirus combined antigen.

(first entry)

23-MAR-1998

Human, cytomegalovirus, combined antigen, detection, antibody, vaccine, immunoglobulin A; IgA.

Human cytomegalovirus. Synthetic.

WO9731117-A2

28-AUG-1997

97WO-EP000865. 20-FEB-1997; 96US-00605541. 22-FEB-1996;

(UYMA-) UNIV MAASTRICHT

WPI; 1997-435169/40. N-PSDB; AAT79194.

Bruggeman CA, Vink C,

Ramon A;

Stals F,

Combined antigen containing parts of 3 human cytomegalovirus proteins useful for early detection of virus specific antibodies and in

Example 4; Page 21; 26pp; English.

preventative vaccines.

The present sequence represents a human cytomegalovirus combined antigen, which contains amino acid sequences from at least 3 human cytomegalovirus (hCMV) proteins and has an increased ability to bind hCMV specific antibodies (AB). The device is used to detect and quantify Ab. particularly of immunoglobulin A (IgA) type, in human body fluids and tissues. The antigen is also used in vaccines for protection against combined antigen can detect hCMV infection at an early stage (allowing early treatment), since sensitivity and accuracy are improved by the interaction of immunodominant regions of early formed proteins present in a single antigen (the combine antigen) a binding ability is 2.3 times greater than for single antigens). The combined antigen also avoids the lack of antigen standardisation which limits use of conventional assay systems

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Gaps

0;

90.6%; Score 48; DB 2; Length 10; 100.0%; Pred. No. 0.091; ive 0; Mismatches 0; Indels

9; Conservative

Matches

Query Match Best Local Similarity

1 TPRVTGGGA 9

1 TPRVTGGGA

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                                                                                                                                                                                                                                                                                                            Immunogenic epitope; human cytomegalovirus; HCMV; vaccine; generic; CD8+; cytotoxic T-lymphocyte; MHC; major histocompatibility complex; CTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present generic peptide sequence is based on the sequence given in AM48885. Sequence variants of the present peptide are recognised by the CD8+ class I major histocompatibility complex (MHC) restricted cyctocoxic T-1ymphocytes of patients harboring latent HCMV infection. The peptides are claimed to be capable of activating cytocoxic T-cell lymphocytes in the absence of active viral reppication, and thus are useful for eliciting a cellular immune response against HCMV by normal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunodeficient subjects. These immunological peptides can also be formulated as vaccines which are claimed to be useful for protecting against HGMV infection, augmenting the immune system response to a HGMV infection or protecting against reactivation of a latent HGMV infection
                                                                                                                                                                                                                                                                            Generic immuno-reactive peptide CTL epitope 4 of human cytomegalovirus.
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoreactive human cytomegalovirus epitopes - useful to vaccinate
                                0;
100.0%; Score 53; DB 2; Length 631; 100.0%; Pred. No. 0.98; o; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Leu, Phe, Met
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                 AAW48986 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 48; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-00950064.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US020236
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                                                                                                                                                                                                                                             (first entry)
Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                 163 TPRVTGGGAM 172
                                                                1 TPRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CITY ) CITY OF HOPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               York J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-297862/26.
                                                                                                                                                                                                                                                                                                                                                                                 Human herpesvirus 5.
                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               against infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9821233-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1996;
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                                                                                                                                                                                                                                               29-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diamond DJ,
                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                AAW48986;
                                                                                                                                                 RESULT 16
                                                                                                                                                                  AAW48986
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us-10-697-055-7.rag

components of antiviral vaccines and to expand immune effector cells

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WPI; 2001-596936/67.
  WPI; 1997-535849/49.
                                                                                                                                                                                     N-PSDB; AAD18185.
                                                                   Sequence 551 AA;
     N-PSDB; AAT91282
                                                                                                                                       Cytomegalovirus
                                                                                                                                             WO200170766-A2
                                                                                                                                                                            Nicolette CA;
                                                                                                                   18-DEC-2001
                                                                                                                                                   27-SEP-2001
              induce an
                infection
                                                                                                              AAE10840;
                                                                         Query Match
                                                                                                      AAE10840
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417 TPRVTGGGAM 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 560 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200163286-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB86545;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                          This sequence comprises the full-length human cytomegalovirus (HCWV) Towne strain tegument phosphoprotein pp55; the strain AD169 pp65 sequence is given in AAW26732. The invention provides DNA molecules (see AAF191280-83 and AAT99436) useful for in vitro and in vivo expression of antigenic fragments of the HCMV genome. Preferred antigens include full-length and transmembrane-deleted fragments of gB (see AAW21274) such as gB1-680, phosphoprotein pp65 (see AAW27276) phosphoprotein pp65 (see AAW27277) and the Ir-exon 4 product (see AAW27275). The DNA molecule is preferably in the form of a plasmid and includes a regulatory sequence for expressing the antigen in mammals, where the antigen elicits an immune response. The products can induce HCMV-specific immune responses including neutralising antibodies and cytotoxic I lymphocytes and can be used for the prevention and treatment of HCMV infections
New human cytomegalovirus DNA constructs - encode a HCMV antigen to induce an immune response, used for the treatment and prevention of {\rm HCMV}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytomegalovirus; CMV; pp65 antigen; cytostatic; virucide; cell therapy; vaccine; viral infection; immunotherapy; gene therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 53; DB 2; Length 551; 100.0%; Pred. No. 0.85; tive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytomegalovirus antigen pp65 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE10840 standard; protein; 560 AA.
                                                                                                                                        Example 3; Fig 5; 66pp; English.
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12-DEC-2000; 2000US-0254989P.
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TPRVTGGGAM 10
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Novel synthetic antigenic compounds useful as components of antiviral vaccines and to expand immune effector cells which are specific for viral infections characterized by expression of cytomegalovirus antigen pp65.

The invention relates to synthetic antigenic compounds which are useful

Claim 7; Page 63-64; 66pp; English.

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specific for viral infections characterised by expression of COMP.

Cytomegalovirus antigen pp65. Antigenic compounds are useful for immunotherapy and also for inducing an immune response in a subject. The antigenic compound is useful for addilating immune response to the cartification of comparts and their corresponding native proteins, and is useful as compound is useful for modulating immune response to the cognate native ligands and their corresponding native proteins, and is useful as compounds and their corresponding native proteins, and is expanding immune effector cells that are specific for viral infections characterised by expression of CMV antigen pp65. Furthermore, the cartigenic compound also has diagnostic applications. The DNA encoding the antigenic compounds are useful as probes and primers for detecting genes antigenic compounds are useful as probes and primers for detecting genes or gene transduction of the polynuclectides into host cells and also in gene therapy techniques for treating cancer. The antigenic compounds immune receptor cell is also useful as vaccines. The antigenic compounds immune receptor cell for preparing medicaments for diseases such as cancer. The present sequence is native CMV antigen pp65 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cells for the immuno-stimulation of mammals and the determination of the response to an antigen (1). The method comprises (i) dividing the amino acid sequence of the antigen into protein fragments (II) of at least 9 amino acids, whereby adjacent or neighbouring fragments are in the whole antigen sequence; (ii) synthesizing a peptide library containing (II); and (iii) incubating the CDB and/or CD4 T lymphocytes in a suspension comprising (II) in a single culture vessel. The method is used to immuno-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigen-specific stimulation, T-lymphocyte, CD8 stimulation, pp65; CD4 stimulation; immuno-stimulation, IB1; lower matrix phosphoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a novel method for stimulating CD8 or CD4 T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the determination of the response to the antigen comprises using a synthetic peptide library of the specific antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytomegalovirus strain AD169 pp65 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Volk H, Reinke P, Faulhaber N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB86545 standard; protein; 561 AA.
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The invention relates to a novel isolated peptide comprising one or more cytotoxic T-lymphocyte (CTL) epitope(s) of the same or different antigen of a human cytomegalovirus (HCMV). The HCMV antigens can comprise pp28, pp50, pp65, pp71, pp150, gB, gH, lE-1, lE-2, US2, US3, US6, US11 or UL18. The peptide comprises a sequence of about 9-20 contiguous amino acids of treating cytomegalovirus infection in humans, and in monitoring immune responses in various clinical settings (e.g. transplantation or pregnancy). This sequence represents a human cytomegalovirus CTL epitope peptide of the invention
                            Virucide; immunostimulant; cytotoxic T-lymphocyte; CTL; epitope; antigen; human cytomegalovirus; HCMV; pp28; pp50; pp65; pp71; pp150; gB; gH; IE-1; IE-2; US2; US3; US6; US11; UL18; cytomegalovirus infection; pregnancy;
                                                                                                                                                                                                                                                                                                                                                                 New human cytomegalovirus (CMV) cytotoxic T-cell epitope peptide, useful for diagnosing, preventing or treating CMV infection, comprises pp28, pp50, pp71, pp150, gB, gH, IR-1, IE-2, US2, US3, US6, US11 or UL18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCMV; CMV; antigen; infection; therapy; vaccine; tegument protein;
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Human cytomegalovirus CTL epitope peptide SEQ ID No 88.
                                                                                                                                                                                                                                                                       (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytomegalovirus tegument protein pp65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "encoded by AAT"
                                                                                                                                                                                                                                                                                                        Walker SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 106; 308pp; English.
                                                                                                                                                                                                             26-JUN-2002; 2002WO-AU000829.
                                                                                                                                                                                                                                           26-JUN-2001; 2001AU-00005931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                        Elkington RA,
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                                                                                                               Human cytomegalovirus.
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Les 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphoprotein pp65
                                                                                                                                                                                                                                                                                                                                      WPI; 2003-300379/29.
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                                                                                                                                             WO2003000720-A1.
                                                                                transplantation.
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                                                                                                                                                                             03-JAN-2003
                                                                                                                                                                                                                                                                                                        Khanna R,
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AD169 strain tegument phosphoprotein pp55; the strain Towne pp65 sequence is given in AAW27276. The invention provides DNA molecules (see AAT91280-83 and AAT99436) useful for in vitro and in vivo expression of antigenic fragments of the HGWV genome. Preferred antigens include full-length and transmembrane-deleted fragments of gB (see AAW27274) such as gB1-680, phosphoprotein pp65 (see AAW27276 and AAW27274) such as gB1-680, (see AAW27277) and the IE-exon 4 product (see AAW27275). The DNA molecule is preferably in the form of a plasmid and includes a regulatory sequence for expressing the antigen in mammals, where the antigen elicits an immune response. The products can induce HGWV-specific immune responses including neutralising antibodies and cytotoxic T lymphocytes and can be used for the prevention and treatment of HGWV infections
                                                                                                                                                                                     New human cytomegalovirus DNA constructs - encode a HCMV antigen to induce an immune response, used for the treatment and prevention of {\rm HCMV}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                   This sequence comprises the full-length human cytomegalovirus (HCMV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HCMV; CMV; antigen; infection; therapy; vaccine; tegument protein;
phosphoprotein pp65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 53; DB 2; Length 551; 100.0%; Pred. No. 0.85;
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                                                                         (WIST-) WISTAR INST ANATOMY & BIOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW27276 standard; protein; 551 AA
                                                                                                         Kari C;
                                                                                                                                                                                                                                                      Example 3; Fig 5; 66pp; English
                                                                                                                                                                                        New human cytomegalovirus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0015717P.
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             97WO-US006866
                                        96US-0015717P
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                         Berencsi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 TPRVTGGGAM 416
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                                                                                                                                         WPI; 1997-535849/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 468
                                                                                                                                                        N-PSDB; AAT99436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 551 AA;
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             22-APR-1997;
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                                                                                                         Gonczol E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW27276;
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Kari

Berencsi K,

Gonczol E,

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AAB86672 standard; peptide; 15 AA.

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Gaps

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This sequence represents a novel method for stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and the determination of the response to an antigen (I). The method comprises (i) dividing the amino acid sequence of the antigen into protein fragments (II) of at least 9 amino acids, whereby adjacent or neighbouring fragments are in the whole antigen sequence; (ii) synthesizing a peptide library containing (II); and (iii) incubating the CD8 and/or CD4 T lymphocytes in a suspension comprising (II) in a single culture vessel. The method is used to immunosimulate T cells of mammals, particularly humans, and is also useful for diagnostic purposes to determine if a mammal, especially human, has previously immunologically responded to a specific protein, and to determine strength of that response. The method is suitable for in wive or in vitro immuno-erimination of mammalian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or in vitro immuno-stimulation of mammalian, more preferably human T lymphocytes, where the stimulated T lymphocytes are expanded and can be transfused into a patient. AAB8654-AAB86803 represent fragments of the human cytomegalovirus IE1 and pp65 lower matrix phosphoprotein which are used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and the determination of the response to the antigen comprises using a synthetic peptide library of the specific antigen.
                                                                                                                                                                                                                                                                                                                                                                                 Antigen-specific stimulation; T-lymphocyte; CD8 stimulation; pp65; CD4 stimulation; immuno-stimulation; IE1; lower matrix phosphoprotein.
                                                                                                                                                                                                                                                                                                                                       Human cytomegalovirus strain AD169 pp65 peptide fragment SEQ ID 130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Khatamzas
100.0%; Score 53; DB 2; Length 15; 100.0%; Pred. No. 0.019; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Surel I,
                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Faulhaber N,
                                                                                                                                                                                                                         AAB86673 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Fig 2; 85pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-FEB-2000; 2000DE-01009341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-FEB-2001; 2001WO-EP001773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reinke P,
                       Best Local Similarity 100.
Matches 10; Conservative
                                                                                  1 TPRVTGGGAM 10
                                                                                                                        3 TPRVTGGGAM 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cytomegalovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kern F, Volk H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200163286-A2.
                                                                                                                                                                                                                                                                                                            20-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-AUG-2001
                                                                                                                                                                                                                                                                   AAB86673;
        Query Match
                                                                                                                                                                                       RESULT 8
                                                                                                                                                                                                          AAB86673
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This sequence represents a novel method for stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and the determination of the response to an antigen (I). The method comprises (i) dividing the amino caid sequence of the antigen into protein fragments (II) of at least 9 caid sequence of the antigen into protein fragments are in the whole antigen sequence; (ii) synthesizing a peptide library containing (II); comprising (II) in a single culture vessel. The method is used to immunocomprising (II) in a single culture vessel. The method is used to immunocomprising (II) in a single culture vessel. The method is used to immunocomply immunologically particularly humans, has diagnostic purposes to determine if a mammal, especially human, has consisted in vitro immuno-stimulation of mammalian, more preferably human T con in vitro immuno-stimulation of mammalian, more preferably human T con in vitro immuno-stimulation of mammalian, more preferably human T con in vitro immuno-stimulation of mammalian, more preferably human T con in vitro immuno-stimulation of mammalian, more preferably human T con in vitro patient. AAB86544AAB86803 represent fragments of the human cytomegalovirus IEI and pp65 lower matrix phosphoprotein which are used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and the determination of the response to the antigen comprises using a synthetic peptide library of the specific antigen.
                                                                                                                         Antigen-specific stimulation; T-lymphocyte; CD8 stimulation; pp65; CD4 stimulation; immuno-stimulation; IE1; lower matrix phosphoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                   Human cytomegalovirus strain AD169 pp65 peptide fragment SEQ ID 129.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Reinke P, Faulhaber N, Surel I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABJ38030 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                     17-FEB-2001; 2001WO-EP001773.
                                                                                                                                                                                                                                                                                                                                       22-FEB-2000; 2000DE-01009341
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Best Local Similarity 100.
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                                                                                                                                                                                      Human cytomegalovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Volk H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                 (KERN/) KERN F.
                                                                                                                                                                                                                              WO200163286-A2.
                                                       20-NOV-2001
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                 AAB86672;
                                                                                                                                                                                                                                                                                                                                                                                                                       Kern F,
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BXXXEX
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0; Gaps

100.0%; Score 53; DB 4; Length 15; 100.0%; Pred. No. 0.019; Live 0; Mismatches 0; Indels

Query Match Best Local Similarity 100. Matches 10; Conservative

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0; Mismatches

related Kaposi's sarcoma, sarcomas, osteosarcoma, renal carcinoma, and haematopoietic malignant tumours such as leukaemia and lymphoma. The aptitope is an HLA, (human leukocyte antigen) peptide derived from a viral orlumour antigen. The present sequence is a viral HLA epitope used in the fusion proteins of the invention

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New polynucleotide capable of expressing an epitope-beta2m fusion protein useful for generating cytotoxic I lymphocyte responses against a tumor and in restoring antigen presentation in the tumor of a host.
sequence is an HCMV pp65 protein immunogenic epitope upon which vaccines and peptides of the invention are based
                                                                                                                                                                                                                                                                                                                                                                                                                                prostatic cancer; testicular cancer; lung cancer; breast cancer; malignant melanoma; mesothelioma; brain tumour; ovarian cancer; uterine cancer; cervical cancer; head and neck cancer; bladder cancer; Kaposi's sarcoma; renal carcinoma; leukaemia; lymphoma; acquired immunodeficiency syndrome; AIDS-related lymphoma.
                                                                                                                                                                                                                                                                                                                                                                      Beta-2 microglobulin; beta-2m; cytotoxic T lymphocyte; CTL; HLA; human leukocyte antigen; fulsion protein; epitope; cytostatic; tumour; gastrointestinal tumour; colorectal cancer; gastro-oesophageal cancer; liver cancer; biliary trac cancer; pancreatic cancer; vaccine;
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tafuro S, Meier U, Mcmichael AJ, Bell JI, Layton G, Hunter M;
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0
                                                                                                                                                                                                                                                                                                                                         Cytomegalovirus lower matrix protein pp65 HLA-B0702 epitope.
                                                                             100.0%; Score 53; DB 5; Length 10; 100.0%; Pred. No. 0.012; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                   ABG66768 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-2001; 2001WO-GB004844.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ISIS-) ISIS INNOVATION LTD.
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                                                                                                             10; Conservative
                                                                                                                                            1 TPRVTGGGAM 10
                                                                                                                                                                          1 TPRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cytomegalovirus.
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                                                                                               Best Local Similarity
                                                  Sequence 10 AA;
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                                                                                 Query Match
                                                                                                                Matches
                                                                                                                                                                                                                   RESULT 6
ABG66768
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The present invention describes a method of inducing and/or sustaining an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The method comprises: (a) delivering an antigen to the mammal at a level to induce an immunological CTL response in the mammal; and (b) maintaining the level of the antigen in the mammal's lymphatic system to maintaining the level of the antigen in the method can be used for the delivery of e.g. a differentiation antigen, a tumour-specific multilineage antigen, an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor gene antigen, or a viral antigen. They can be used for the treatment of antigen, or a viral antigen. They can be used for the treatment of antigen, as cancer, e.g. malignant melanoma or infectious disease, e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery to the lymphatic system provides for potent CTL stimulation that takes place in the milieu of the lymphoid organ, and it sustains stimulation the takes place in the milieu of the lymphoid organ, and it sustains stimulation the black of air and the bresent invention
                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inducing a cytotoxic T lymphocyte response - by maintaining a level of antigen in the lymphatic system of a mammal so as to provide a sustained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system; immunisation; tumour; infectious disease; immunotherapy; cancer; malignant melanoma; viral disease; hepatitis; AIDS.
                                                                                                                                                                             0;
                                                                                                                                       100.0%; Score 53; DB 5; Length 10; 100.0%; Pred. No. 0.012; ive 0; Mismatches 0; Indels
                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        T cell epitope/MHC ligand SEQ ID NO:148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTL response, used to treat, e.g. AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 29; 199pp; English
                                                                                                                                                                                                                                                                                                                                             AAY10218 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CTLI-) CTL IMMUNOTHERAPIES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97CA-02209815.
97US-00988320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US014289
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                                                                                                                                                                             10; Conservative
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                                                                                                                                                                                                                 1 TPRVTGGGAM 10
                                                                                                                                                                                                                                                      1 TPRVTGGGAM 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human herpesvirus 5.
                                                                                                                                                            Best Local Similarity
                                                                                                       Sequence 10 AA;
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10-DEC-1997;
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                                                                                                                                           Query Match
                                                                                                                                                                                 Matches
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Sequence 15 AA;

The invention relates to a new polynuclectide capable of expressing an epitope-beta 2m fusion protein useful for generating cytotoxic T

Iymphocyte (CTL) responses against a tumour or in restoring antigen presentation in the tumour of a host. Also included are a polynuclectide capable of expressing an epitope-beta 2m fusion protein in combination with a vaccination agent that stimulates a CTL response against the epitope of the fusion protein for simulates a CTL response against the use in the treatment of cancer and a method of treating a tumour by administering a capable of expressing an epitope-beta 2m fusion protein, and optionally a vaccination agent that stimulates a CTL response against the epitope of the fusion protein. The polynucleotide is useful for the epitope of the fusion protein. The polynucleotide is useful for generating CTL responses against tumours, for restoring antigen protein in the tumour, and subsequently for treating cancers, such as gastrointeerinal tumour, protatic, testicular, lung or breast cancer, malignant melanoma, mesotheliona, brain tumour, ovarian cancer, uterine cancer including cervical cancer, cancer of the head and neck, bladder cancer, Kaposi's sarcoma, AIDS (acquired immunodeficiency syndrome)-

Disclosure; Page 24; 46pp; English.

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Gaps

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0; Indels

100.0%; Score 53; DB 4; Length 10; 100.0%; Pred. No. 0.012;

0; Mismatches

10; Conservative 1 TPRVTGGGAM 10 1 TPRVTGGGAM 10

à

Best Local Similarity

Query Match Matches

Sequence 10 AA;

a cellular immune response against HCMV by normal and immunodeficient subjects. The peptides may be used in an assay for determining the degree of immunostimulation caused by HCMV. The peptides may also be used for distinguishing individuals who are seropositive from those who have not been exposed to HCMV (seronsgarive individuals). The present peptide sequence is a minimal cytotoxic epitope from human cytomegalovirus. This sequence has allele specificity to HLA B7 and subtypes

8\$8888888\$\$

activating CTLs and CTL precursors (CTLp), particularly for eliciting

New peptides that are immunogenic epitopes of the human cytomegalovirus (CMV), useful for activating cytotoxic T lymphocytes (CTL) or CTL precursors to elicit an immune response against human CMV by normal or 27-MAR-2000; 2000US-00534639. immunodeficient subjects. (DIAM/) DIAMOND D J. York J; WPI; 2001-431950/46. YORK J. US6251399-B1. 12-NOV-1996; 11-MAY-1998; Diamond DJ, 10-FEB-1998; 24-SEP-2001 26-JUN-2001 AAE05431; (YORK/) Matches RESULT 888888888888888 à

0 useful for imparting immunity to a bone marrow transplant recipient, a solid organ recipient, a heart patient, an AIDS patient or a woman of child-bearing years, without the need for ex vivo expansion of HCWV-specific CTL. These peptides can directly stimulate cytotoxic T lymphocytes (CTL) in vitro, thus can be used in an assay to determine the degree of immunostimulation caused by HCMV. These may also be used to distinguish individuals who are seropositive from those who have not been exposed to HCMV and in the study of the Class I antigen-processing pathway for HCMV proteins. The present sequence represents a peptide used in the exemplification of the present invention and is at risk for reactivation of HCMV infection. The peptides are also 0; Gaps Human cytomegalovirus; HCMV; cytotoxic epitope; infection; vaccine; cytotoxic T lymphocyte; CTL; CTL precursor; CTLp; Class I antigen; major histocompatibility complex; MHC; cellular immune response; CTL activator; CTLp activator; immunostimulant. Human cytomegalovirus (HCMV) minimal cytotoxic epitope #3. 100.0%; Score 53; DB 3; Length 10; 100.0%; Pred. No. 0.012; 0; Indels 0; Mismatches AAE05431 standard; peptide; 10 AA. (first entry) 10; Conservative 1 TPRVTGGGAM 10 1 TPRVTGGGAM 10 Human cytomegalovirus. Query Match Best Local Similarity Sequence 10 AA;

AAU10826 standard; peptide; 10 AA.

RESULT 5 AAU10826

The invention relates to immunogenic peptides derived from human cytomegalovirus (HCMV) which are recognised by human cytotoxic T
[Very promegalovirus (HCMV) which are recognised by human cytotoxic T
[Very promedalovirus (HCMV) which are recognised by human cytotoxic T
[Very peptide of the peptides, and a pharmaceutically acceptable

[Very peptide of the vaccine against HCMV comprising antigan presenting

[Very peptide of the vaccine is used to modulate the immune response to human

[Very peptide of the vaccine is used to modulate the immune response to human

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[Very peptide of the immune of its ease and other interval is used to modulate the immune of its ease and other interval is used to modulate the immune of its ease and other interval is used to modulate the immune of its ease and other is used to modulate the immune of its ease and other is used t New immunogenic peptides useful as a vaccination against cytomegalovirus infection, comprises epitopes of human cytomegalovirus which are recognized by human cytotoxic T-lymphocytes. virucide; restenosis; coronary angioplasty; morbidity; mortality; AIDS; acquired immunodeficiency syndrome; viral retinitis; blindness; encephalitis; enteritis; mononucleosis; interstitial pneumonia; malignancy; Karposi's sarcoma; post-bone marrow transplant complication. mmunogenic epitope; pp65; cytotoxic I cell; CLL; HCMV; vaccine; Human cytomegalovirus pp65 protein immunogenic epitope #4. Claim 12; Page 28; 65pp; English 27-MAR-2000; 2000US-00534639. 20-OCT-2000; 2000US-00692170. 16-MAR-2001; 2001WO-US008576. (first entry) Human cytomegalovirus. (CITY) CITY OF HOPE. WPI; 2002-041233/05. WO200172782-A2. 14-FEB-2002 04-OCT-2001 Diamond DJ; AAU10826;

> 96US-007474BB. 98US-00021298.

98US-00075257

The invention relates to immunologically active peptides, and functional variants thereof, capable of eliciting a cellular immune response to thuman cytomegalovorius (HGMV) in humans. The peptides are capable of directing human cytotoxic T lymphocytes (CTL) to recognise and lyse human cells infected with HCMV. Such immunologically active peptides, in association with an major histocompatibility complex (HCC) class I molecule, are recognised by CTLs of individuals having a latent (inactive) HCMV infection. Vaccines comprising these peptides are useful

Example 14; Col 7; 17pp; English.

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Immunoreactive human cytomegalovirus epitopes - useful to vaccinate
                                           against infection.
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Claim 9; Page 49; 56pp; English.

The present peptide is an immunogenic epitope which is recognised by the CD8+ class I major histocompatibility complex (MHC) restricted cytotoxic T-lymphocytes of patients harboring latent HCMV infection. The peptide is claimed to be capable of activating cytotoxic T-cell lymphocytes in the absence of active viral replication, and thus is useful for eliciting a cellular immune response against HCMV by normal and immunodeficient subjects. The immunological peptide can also be formulated as a vaccine which is claimed to be useful for protecting against HCMV infection, which is claimed to be useful for protecting against HCMV infection, augmenting the immune system response to a HCMV infection or protecting against reactivation of a latent HCMV infection

Sequence 10 AA;

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0; Gaps
100.0%; Score 53; DB 2; Length 10; 100.0%; Pred. No. 0.012; tive 0; Mismatches 0; Indels
                           Best Local Similarity 100.
Matches 10; Conservative
           Query Match
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1 TPRVTGGGAM 10 1 TPRVTGGGAM 10 à

RESULT 2 AAY09322

AAY09322 standard; peptide; 10 AA.

AAY09322;

08-JUL-1999

Immunogenic peptide cytotoxic T lymphocyte epitope SEQ ID NO:7 of hCMV.

(first entry)

immune response; cytotoxic T lymphocyte; CTL; immunostimulation; infection; immunosuppression; bone marrow transplant; solid organ; heart; Human cytomegalovirus; hCMV; immunologically active peptide; vaccine;

Human herpesvirus 5.

Synthetic.

WO9919349-A1 22-APR-1999 98WO-US009652. 11-MAY-1998; 97US-00950064. L4-OCT-1997; LO-FEB-1998;

(CITY) CITY OF HOPE.

Diamond DJ,

WPI; 1999-277590/23

Immunogenic peptide cytotoxic T lymphocyte epitopes of human cytomegalovirus.

Claim 9; Page 50; 64pp; English.

capable of eliciting a cellular immune response to human cytomegalovirus (hCMV). The IAP can be used in a (cellular) vaccine to augment the immune system response to HCMV, or to provide immunity against HCMV. The IAP cellular vaccine can also protect an individual having a latent HCMV infection from reactivation. An antigen presenting cell can be used to determine the presence or absence of HCMV-infected T lymphocytes. The viral vector containing IAP encoding DNA can also be used to provide present invention describes immunologically active peptides (IAPs)

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The present invention describes a cellular vaccine (I), which elicits a MHC class I cellular immune response to human cytomegalovirus (HCWV), and comprises a peptide selected from (i) - (v), provided that (i) is not another peptide (vi): (i) Asn Xaal Vall Pro Met Val Ala Thr Xaa2; (ii) Tyr Xaa3 Glu His Pro Thr Phe Ser Gln Tyr; (iii) Phe Xaa4 Phe Pro Lys Asp Val Ala Leu Xaa5; (iv) Thr Pro Arg Val Thr Gly Gly Gly Gly Ala Xaa5; and (v) Phe Pro Thr Lys Asp Val Ala Leu, where: Xaa1 = Leu, Ile, Met, Thr or Val; Xaa2 = Val, Ala, Cys, Ile, Leu or Thr; Xaa3 = Ser, Thr or Leu; Xaa4 = Val or Thr; Xab5 = Leu, Arg or Lys; Xaa6 = Leu, Met or Phe; and (i) is not Asn Leu Val Pro Met Val Ala Thr Val (vi). The peptides are useful is not providing immunity against future infections by HCMV, and for augmenting the immune response of an individual who is latently infected with HCMV
                                                                                                                                                                                                                                                                                                                                      o;
immunity against HCMV. The IAP can be used to prepare HCMV-reactive human cytocoxic T lymphocytes. The antigen presenting cells primed with the IAPs can be used as diagnostic reagents to detect immunostimulation by HCMV. They can also detect active HCMV infection or exposure to HCMV.
                                                                                 HCMV can cause opportunistic infections resulting in a variety of complications in, e.g. immunosuppressed patients. The IAP vaccines impart immunity to bone marrow transplant recipients, solid organ recipients, heart patients, AIDS patients or women of child-bearing years, without the need for ex vivo expansion of HCMV-specific cytotoxic T lymphocytes (which requires sophisticated laboratory setup and is highly labor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New immunogenic peptides useful for providing immunity against cytomegalovirus (CMV) infections, are capable of eliciting cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic; cytotoxic T lymphocytes; CTL; cytomegalovirus; HCMV; infection; immune response; vaccine; immunostimulant; antiviral; immunosuppressive; immunity; immunisation.
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                                                                                                                                                                                                                                                                                             100.0%; Score 53; DB 2; Length 10; 100.0%; Pred. No. 0.012; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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2 PRVTGGG 8
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; Sequence 66952, Application US/10425114
; Dublication No. USZ0040034888A1
; GENERAL INFORMATION:
    APPLICANT: Liu, Jingdong
    APPLICANT: Shou, Yihua
    APPLICANT: Screen, Steven E
    APPLICANT: Tabaska, Jack E
    APPLICANT: Tabaska, Jack E
    APPLICANT: APPLICANT: Pabaska, Jack E
    APPLICANT: APPLICANT: Pabaska, Jack E
    APPLICANT: APPLICANT: APPLICANT: APPLICANT: Cao, Yongwei
    TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
    FILE REFERENCE: 38-21(53313) B
    CURRENT APPLICATION NUMBER: US/10/425,114
    CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 66952
    LENGTH: 383
    MANDER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                Sequence 2, Application US/09895593

Sequence 2, Application US/09895593

Sequence 2, Application US/09895593

Sequence 2, Application US/09895593

SENERAL INFORMATION:

APPLICANT: Baumann, Heinz

APPLICANT: Baumann, Heinz

APPLICANT: Econach, Warren D.

APPLICANT: Leonach, Warren J.

APPLICANT: Leonach, Warren J.

APPLICANT: Leonach, Warren J.

APPLICANT: Leonach, Warren J.

TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and

TITLE OF INVENTION: Uses Thereof

FILE REFERENCE: 00-514-E

CURRENT FILING DATE: 2000-06-28

FRICK FILING DATE: 2000-06-28

NUMBER: OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 370

TURE NOS: DATE: DATE

LENGTH: 370
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                          2; Indels
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US-10-425-114-66952
Pred. No. 6e+02;
0; Mismatches
     77.8%;
  Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                           344 PRGPGGGAM 352
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                                                                            2 PRVTGGGAM 10
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ORGANISM: Zea mays
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Cy 2 PRYTGGG 8

BD B7 PRASGGG 93

RESULT SO

US-09-835-684-9

Sequence 9, Application US/09835684

| PRASEAL INFORMATION:
| APPLICANT: 0iu, Dewen |
| TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR |
| TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR |
| TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR |
| TITLE OF INVENTION: DESICCATION NUMBER: 06/198/359 |
| TITLE OF INVENTION: 2000-04-16 |
| PRIOR RAPHICANTON NUMBER: 06/198/359 |
| TITLE OF INVENTION: 2000-04-19 |
| TITLE OF INVENTION: 2000-04-16 |
| TITLE OF INVENTION: 2000-04-19 |
| TITLE OF INVENTION: 2000
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us-10-697-055-7.rapb

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SEQ ID NO 7
LENGTH: 361
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; Sequence 3, Application US/09895593
; Patent No. US20020160949A1
; GENERAL INFORMATION:
; APPLICANT: Panday, Akhilesh
; APPLICANT: Baumann, Heinz
; APPLICANT: Baumann, Heinz
; APPLICANT: Econach, Warren D.
; APPLICANT: Ziegler, Steven F.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and
; TITLE OF INVENTION: Uses Thereof
; TITLE OF USERNICE: 00-514-E
; CURRENT APPLICATION NUMBER: US/09/895,593
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APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Thymic Stronal Lymphopoietin Receptor Molecules and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-514-C
CURRENT PEDILICATION NUMBER: US/09/895,943
CURRENT FILING DATE: 2001-06-28
PRIOR PILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN NOSE: 200
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                                                                                                                                                                          Length 338;
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                                                                                                               CTHER INFORMATION: Orthologous to G1652 US-10-374-780A-1701
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PRIOR APPLICATION NUMBER: 60/215,658
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                US-09-895-943-3

'Sequence 3, Application US/09895943

; Patent No. US20020068323A1

; GENERAL INFORMATION:
SOFTWARE: PatentIn version 3.2
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Best Local Similarity 77.6
Best Local 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , NAME/KEY: TRANSMEM
; LOCATION: (227)..(247)
US-09-895-943-3
                                                          TYPE: PRT
ORGANISM: Oryza sativa
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91 SPHVTGGG 98
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LENGTH: 353
TYPE: PRT
                  SEQ ID NO 1701
LENGTH: 338
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APPLICANT: Saris, Chris
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-514-C
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                                                                                                                                                                                                                                   66.0%; Score 35; DB 9; Length 353; 77.8%; Pred. No. 5.7e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7. Application US/10226872;
Publication No. US2003015711841
GENERAL INFORMATION:
APPLICANT: Cabezon-Silva, Teresa Elisa Virginia
APPLICANT: Cache, Thierry
APPLICANT: Gaulis, Swann Romain Jean-Thomas
APPLICANT: Vinals Y De Bassols, Carlota
APPLICANT: Vinals Y De Bassols, Carlota
APPLICANT: Cassart, Jean-Poll
APPLICANT: Cassart, Jean-Poll
CANTER OF INVENTION: Tumour-Specific Animal Proteins
FILE REFERENCE: BC45300-1
CURRENT APPLICANION UNMBER: US/10/226,872
CURRENT FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 33
SOFFWARE: FRSESQ for Windows Version 3.0
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CURRENT FILING DATE: 2001-06-28
PRIOR PPLICATION NUMBER: 60/214,866
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 370
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Sequence 2, Application US/09895943

Patent No. US20020068323A1

GENERAL INFORMATION:
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 353
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Best Local Similarity 77.0.
To Conservative
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                                                                                                                                                                                                                                                                                                                                         2 PRVTGGGAM 10
                                                                          TYPE: PRT ORGANISM: Mus musculus
                                                                                                                       FEATURE:

NAME/KEY: TRANSMEM

LOCATION: (227)...(247)

US-09-895-593-3
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US-10-226-872-7
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APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
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Pred. No. 5.4e+02;
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                                                             APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: BATTORI, MASAHIRA
TILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9249
LENGTH: 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2003-02-25
PRIOR FILING DATE: 2001-04-18
PRIOR PELING DATE: 2001-04-18
PRIOR PELING DATE: 2001-08-09
PRIOR PELING DATE: 2001-08-09
PRIOR PELING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR PELING DATE: 2001-08-22
PRIOR PELING DATE: 2001-11-19
PRIOR PELING DATE: 2001-12-11
PRIOR PELING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/11,468
PRIOR PELING DATE: 2002-06-14
PRIOR PELING DATE: 2002-06-19
PRIOR PELING DATE: 2002-06-09
PRIOR PELING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Streptomyces avermitilis US-10-156-761-9249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Keddie, James
Broun, Pierre E
Pilgrim, Marsha L
Dubell III, Arnold T
Pineda, Omaira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
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Haake, Volker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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Adam, Luc J
Reuber, T. Lynne
                    ISHIKAWA, JUN
HORIKAWA, HIROSHI
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HARUO
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APPLICANT:
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APPLICANT
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFREENCE: 38-21(53.23)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 220062
LENGTH: 231
                                                                                                             Sequence 206428, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Can vanywei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILLE REFERENCE: 38-21(53223)B

CURRENT APPLICANTON NUMBER: US/10/424,599

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 206428
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Best Local Similarity 60.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

66.0%; Score 35; DB 12; Length 163;

Best Local Similarity 85.7%; Pred. No. 2.7e+02;

Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_40745C.1.pep
US-10-424-599-220062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_28431C.1.pep
US-10-424-599-206428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 220062, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9249, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 rPRITGCGIL 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TPRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 PRVSGGG 81
       21 PRATGGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PRVTGGG 8
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                                                                                                        US-10-424-599-20642B
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US-10-156-761-9249
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Gaps

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MESUL: 3-599-255296

WESUL: 3-599-255296

Sequence 255296, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwai

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

ERROTH: 153
                                                                                                                                                                                                                                                                                   Sequence 258345, Application US/10424599

Sequence 258345, Application US/10424599

Sequence 258345, Application US/10424599

Publication No. US20040031072A1

APPLICANT: La Rosa Thomas J

APPLICANT: Covour Yimus

APPLICAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.0%; Score 35; DB 12; Length 94; 85.7%; Pred. No. 1.5e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                  1; Indels
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US-10-424-599-255296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT3847_7530C.1.pep
US-10-424-599-258345
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66.0%; Score 35; DB 12;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 1;
75.0%; Pred. No. 1.1e+02;
live 1; Mismatches 1
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OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 85.7
Matches 6; Conservative
   Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                       33 SPEVTGGG 40
                                                                                                        1 TPRVTGGG 8
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LENGTH: 94
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Sequence 207115, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: La Royald K

APPLICANT: Cao Yongwel

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 207115

LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 ($2052)
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10058
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87.5%; Pred. No. 9.4e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                             67.9%; Score 36; DB 12; Length 768; 75.0%; Pred. No. 8.4e+02; tive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: magnetite-containing magnetic coccus US-10-369-493-10058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 10058, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                                                NAME/KEY: MISC_FEATURE
1.0CATION: (479)..(479)
1.0CHER INFORMATION: X=any amino acid
US-10-282-1228-45835
                    OTHER INFORMATION: X=any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 87...
1. Conservative
                                                                                                                                                                                                                                                       Query Match 67.9%
Best Local Similarity 75.0%
Matches 6; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                       374 PRIPGGGA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 PRVHGGGA 79
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US-10-424-599-207115
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US-10-369-493-10058
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66.0%; Score 35; DB 12; Length 69;

Query Match

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APPLICANT: Xu, H.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 05/19/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PRIOR DATE: 2001-12-26
PRIOR FILING DATE: 2001-12-26
PRIOR PRIOR DATE: 2001-12-26
PRIOR FILING DATE: 2001-12-26
PRIOR FILING DATE: 2001-12-26
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-03
PRIOR FILING DATE: 2001-02-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MISC_FEATURE
LOCATION: (348)..(348)
OTHER INFORMATION: X=any amino acid
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OTHER INFORMATION: X=any amino acid
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LOCATION: (382\overline{\lambda}..(382)
OTHER INFORMATION: X=any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (114)..(114)
OTHER INFORMATION: X=any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (116)..(116)
OTHER INFORMATION: X=any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (360)..(360)
OTHER INFORMATION: X=any amino acid
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OTHER INFORMATION: X=any amino acid
                           Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bacillus anthracis
Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: MISC FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewn C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20821
LENGTH: 600
                                                          APPLICANT: Zhou, Yihua Zhou, Yereen, Steven E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT PILING DATE: 2003-04-28
SEQ ID NO 70152
LENGTH: 560
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Sequence 45835, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 20821, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
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; ORGANISM: Rhodopseudomonas palustris
US-10-369-493-20821
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Best Local Similarity 100.(
Matches 7; Conservative
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Les 7; Conservative
                               APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
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   GENERAL INFORMATION:
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US-10-369-493-20821
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; Publication No. US20030233675A1
; GERREAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT PAPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16082
                                                                                                                                                                                                                                                                                                        APPLICANT: Gao, Yorgwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Marry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REPRESENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR PLLING DATE: 2003-02-28
PRIOR PLLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15590
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67.9%; Score 36; DB 14; Length 244; 70.0%; Pred. No. 2.7e+02; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 67.9%; Score 36; DB 15; Length 276; Best Local Similarity 66.7%; Pred. No. 3e+02; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                       9 Sequence 15690, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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Best Local Similarity 66 ''',
France 6; Conservative
                    Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                       1 TPRVTGGGAM 10
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    Query Match
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Sequence 15324, Application US/10369493
; Bublication No. US20030233675A1
; Bublication No. US20030233675A1
; Bublication No. US20030233675A1
; Bublicant Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Gladman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: BARRS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: BARRS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; FILE REFERENCE: 2003-02-28
; PRIOR FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Javid K.
APPLICANT: Screen, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: PARSITION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 64171
LENGTH: 346
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US-10-425-114-70152
Sequence 70152, Application US/10425114
; Publication No. US20040034888A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Xanthomonas campestris
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Matches 6; Conservative
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54 TPRMAGGG 61
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ORGANISM: Zea mays
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US-10-425-114-64171
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Query Match 67.9%; Score 36; DB 14; Length 145; Best Local Similarity 77.8%; Pred. No. 1.6e+02; Matches 7; Conservative 0; Mismatches 2; Indels
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.4

OTHER INFORMATION: WISSPROT HIT: 008788, EVALUE 1.60e+00
                             1; Indels
  Pred. No. 60;
3; Mismatches
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI WASAHIRA
TITLE OF INVENTION: NOVEL FOLYNUCLEOTIDES
FILE REFRERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-272697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 15056, Application US/10156761; Publication No. US20030119018A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 Sequence 27829, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
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  60.0%;
                                6; Conservative
                                                                                    1 TPRVTGGGAM 10
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28 SPYMTGGGAL 37
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                RESULT 27
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Sequence 180013, Application US/204003107241

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Car Vorgic
Bapticant: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53233)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DAIR: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                              Query Match 69.8%; Score 37; DB 14; Length 748; Best Local Similarity 75.0%; Pred. No. 5.6e+02; Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.9%; Score 36; DB 12; Length 39; ilarity 75.0%; Pred. No. 44; Conservative 2; Mismatches 0; Indels
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US-10-424-599-180013
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APPLICANT: SHIBA, TADAYCSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNCLEOTIDES
FILE REFERRNCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
SERIOR FILING DATE: 2001-08-02
LENGTH: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.9%; Score 36;
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: ISBIA, HARUO
APPLICANT: ISBIRAM, JUN
APPLICANT: HORIKAWA, HIROSHI
     ; TYPE: PRT
; .ORGANISM: Streptomycem avermitilis
US-10-156-761-12713
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                                                                                                                                                                                                                                                                                       593 PRINGGGA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:|:||||
3 PKVSGGGA 10
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                                                                                                                                                                                                                                2 PRVTGGGA 9
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Best Local Similarity
Matches 6; Conserv
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US-10-156-761-13012
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LENGTH: 39
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hank David R.
APPLICANT: Hank David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: BECHARA ** ADOMINA** ADOMINA** US/10/029,386
CURRENT FILING DATE: 2001-12-20
CURRENT FILING DATE: 2001-12-20
SOFTWARE: Annoman Sequence Listing Engine vers. 1.1
SEQ ID NO 27829
LENGTH: 145
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                                                                                                                                                                                                      69.8%; Score 37; DB 12; Length 121; 77.8%; Pred. No. 91; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Park, Frances
APPLICANT: Bachwala, Ketan S.
APPLICANT: Gajiwala, Ketan S.
APPLICANT: Buchanan, Sean Grant
APPLICANT: Buchanan, Sean Grant
TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF A FLAVIN
TITLE OF INVENTION: MONONUCLEOTIDE BINDING PROTEIN (FMNBP)
FILE REFERENCE: 52498-20011.00
CURRENT APPLICATION NUMBER: US/10/306,762
CURRENT FILLING DATE: 2003-04-16
PRIOR FILLING DATE: 2003-04-16
PRIOR FILLING DATE: 2001-11-28
                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_60138C.1.pep
US-10-424-599-241541
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Sequence 12713, Application US/10156761

Sequence 12713, Application US/10156761

Sequence 12713, Application US/10156761

GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: ISHIKAMA, HIROSHI
APPLICANT: ISHIKAMA, HIROSHI
APPLICANT: SHIBA, TARAYOSHI
APPLICANT: SHIBA, TARAYOSHI
APPLICANT: HATYORI, WOSHIYUKI
APPLICANT: SHIBA, TARAYOSHI
APPLICANT: SHIBA, TABAYOSHI
APPLICANT: SHIBA, TABAYOSHI
CURRENT FILINGE: 249-262
CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30

PRIOR PLING DATE: 2001-05-30

PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 242
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 109
LENGTH: 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 109, Application US/10306762; Publication No. US20030187220A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: C. aurantiacus (22971932)
US-10-306-762-109
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SEQ ID NO 12713
LENGTH: 748
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Best Local Similarity 77.84
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Best Local Similarity 75.0
Matches 6; Conservative
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                                                                               ORGANISM: Glycine max
SEQ ID NO 241541
LENGTH: 121
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US-10-306-762-109
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                                                    TYPE: PRT
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; Sequence 241541, Application US/10424599
; Sequence 241541, Application US/2A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Cav Vongwei
; APPLICANT: Cav Yongwei
; APPLICANT: Cav Yongwei
; APPLICANT: Cav Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With; TITLE OF STUDIATION NUMBER: US/10/424,599
; CURRENT FILLING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILLE REPERSIOR: 38 -21(53231)B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILLING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 232152
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Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 87.5%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_51655C.1.pep
US-10-424-599-232152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 232152, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                              PRIOR APPLICATION NUMBER: 10/225,066
PRIOR FILING DATE: 2002-08-09
PRIOR PILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR PILING DATE: 2002-08-09
PRIOR PILING DATE: 2002-08-09
PRIOR PRIUNG DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PETENTIN VETSION 3.2
SEQ ID NO 2854
LENGTH: 383
                                                                                                                                                                                                                                                                                                                            ORGANISM: Arabidopsis thaliana
           FILING DATE: 2002-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: G2373
US-10-374-780A-2854
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US-10-424-599-241541
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US-10-424-599-232152
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Sequence 74647, Application US/10425114
; Sequence 74647, Application US/200400348881
; Sequence 74647, Application No. US200400348881
; GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
; APPLICANT: Screen, Steven E
; APPLICANT: Screen, Steven E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION NUMBER: US/10/425,114
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NO 70467
; LENGTH: 210
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
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71.7%; Score 38; DB 12; Length 210;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Clone ID: UC-ZMFLM017259F06_FLI.pep
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Publication No. US20040019927A1
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, OSee Luis
APPLICANT: Tang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
APPLICANT: Heard, Volker
APPLICANT: Creelman, Robert A
APPLICANT: Racliffe, Oliver
APPLICANT: Adam, Luc J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR APPLICATION NUMBER: 09/934,655
PRIOR APPLICATION NUMBER: 00/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR PRILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR PULICATION NUMBER: 0/338,692
PRIOR PLICATION NUMBER: 0/319,692
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Dubell III, Arnold T
Pineda, Omaira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reuber, T. Lynne
Keddie, James
Broun, Pierre E
                   7 rPRTIGGGA 15
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 20
US-10-374-780A-2854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-425-114-70467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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APPLICANT: Kovalic David K
APPLICANT: Acade Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 285684
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                                             APPLICANT: Lange, Markus B.
APPLICANT: Glassemian, Majid
APPLICANT: Glassemian, Majid
APPLICANT: Cooper, Bret
APPLICANT: Gooper, Bret
APPLICANT: Gragini, Fumiyaki
APPLICANT: Kregs, Joel
APPLICANT: Kregs, Joel
APPLICANT: Kregs, Joel
APPLICANT: Ricke, Darrell
APPLICANT: Moughamer, Todd
APPLICANT: Micholas
APPLICANT: Alow Tong
APPLICANT: Alow Tong
APPLICANT: Zhu, Tong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.6%; Score 39; DB 15; Length 665; 60.0%; Pred. No. 2.3e+02; tive 3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/259,194A
CURRENT FILING DATE: 2003-01-07
FUND RAPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR FILING DATE: 2002-04-04
PRIOR PLING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 662
NOWARE: PATENTIAL OF SEQ ID NOS: 662
SOFWARE: PATENTIAL OF SEQ ID NOS: 663
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US-10-424-599-269734
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OTHER INFORMATION: unsure at all Xaa locations
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; Publication No. US20040031072A1
; GENERAL INFORMATION:
Publication No. US20040010815A1 GENERAL INFORMATION:
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Best Local Similarity 77.00
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Best Local Similarity 60.vv
G; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Oryza sativa
US-10-259-194A-124
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US-10-424-599-269734
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1 TPRVTGGGA 9

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Herrman, John L
Peyman, John A
Gorman, Linda
Mazes, Peter D
Kekuda, Ramesh
Tanpier Jr, Raymond J
Gerlach, Valerie
                                          Edinger, Shlomit R
MacDougall, John R
Malyankar, Uriel M
Patturajan, Meera
Shimkets, Richard A
Pena, Carol EA
                                                                                                                                                                            Tchernev, Velizar T
Zerhusen, Bryan D
Miller, Isabelle
Miller, Charles E
Lepley, Denise M
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Baumgartner, Jason
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                       Guo, Xiaojia Sasha
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Ellerman, Karen
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Best Local Similarity 75.0
Matches 6; Conservative
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43 PRITGGGS 50
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TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
TITLE OF INVENTION: USING THE SAME
TITLE OF INVENTION: USING THE SAME
FILE REFERENCE: 21402-245
CURRENT APPLICATION NUMBER: US/10/51,874
CURRENT APPLICATION NUMBER: 00/268,595
PRIOR PELING DATE: 2001-02-14
PRIOR PILING DATE: 2001-09-27
PRIOR PILING DATE: 2001-09-27
PRIOR PILING DATE: 2001-01-18
PRIOR PILING DATE: 2001-01-13
PRIOR PILING DATE: 2001-01-13
PRIOR PILING DATE: 2001-01-14
PRIOR PILING DATE: 2001-01-15
PRIOR PILING DATE: 2001-01-16
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US-10-051-874-87
Sequence 87, Application US/10051874
Publication No. US20040005557A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Alsobrook II, John P
APPLICANT: Colman, Steven D
APPLICANT: Spytek, Kimberly A
APPLICANT: Boldog, Ferenc
                                                                  Smithson, Glennda
Baumgartner, Jason C
Herran, John L
Peyman, John A
Gorman, Linda
Mezes, Peter D
                                                                                                                                                                                                      Kekuda, Ramesh
Taupier Jr, Raymond J
Gerlach, Valerie
Grosse, William M
Millet, Isabelle
Miller, Charles E
Lepley, Denise M
                                                                                                                                                                                                                                                                                                Liu, Xiaohong
Ellerman, Karen
Rothenberg, Mark
Stone, David J
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Shenoy, Suresh G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Rattus norvegicus US-10-051-874-86
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43 PRITGGGS 50
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Best Local Similarity
Matches 6; Conserv
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## APPLICANT: Rothernerd, Mark
## APPLICANT: Rothernerd, Mark
## APPLICANT: Stone, David of
## TITLE OF INVENTION: PROTEINS. POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
## TITLE OF INVENTION: PROTEINS. DAVID of
## TITLE OF INVENTION: PROTEINS OF STONE
## TITLE OF INVENTION: OF STONE
## TITLE OF INVENTION: OF STONE
## TITLE OF INVENTION: OF STONE
## TITLE OF INVENTION NUMBER: 06/225,306
## PRIOR APPLICANTON NUMBER: 06/22,409
## RING PRILING DATE: 2001-01-36
## PRIOR PRILING DATE: 2001-01-31
## PRI
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Patturajan, Meera
Shimkets, Richard A
Pena, Carol EA
Tchernev, Velizar T
Zerhusen, Bryan D
      Taylor, Sarah
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43 PRITGGGS 50
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APPLICANT Taylor, Valiar T
APPLICANT Tehernev, Veliar T
APPLICANT Grosse, Milliam M
APPLICANT Grosse, Milliam M
APPLICANT Grosse, Milliam M
APPLICANT Garlach, Valerie L
APPLICANT Baldog, Ference L
APPLICANT Alsobrook II, John P
APPLICANT Rainger, Shomit R
APPLICANT Rainger, Mark E
APPLICANT Rainger, Mark E
APPLICANT Rainger, Mark E
APPLICANT Rochenberg, Mark E
APPLICANT Rochenberg, Mark E
APPLICANT Silerman, Karen
APPLICANT School of Jenda
APPLICANT Schoo
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73.6%; Score 39; DB 12; Length 342;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels
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APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan D; APPLICANT: Sernusen, Stacie J; APPLICANT: Shenoy, Suresh G; APPLICANT: Shenoy, Suresh G; APPLICANT: Spytek, Kimberly
Shenoy, Suresh G
Spytek, Kimberly
Zhong, Mei
Gangolli, Esha A
Burgess, Catherine E
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Gangolli, Esha A
Burgess, Catherine E
                                                                                                                                                       Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
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Vernet, Corine A.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQ ID NO 152
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-042-865-152
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43 PRITGGGS 50
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US-10-042-865-154
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APPLICATION TIGHTON VEHICLE TAPELICATION TIGHTON TO THE TAPELICATION TIGHTON TO THE TAPELICATION TIGHTON TO THE TAPELICATION T
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APPLICANT: MacDougall, John
APPLICANT: Malyankar, Uriel M
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Gunther, Exik
APPLICANTON: Under: US/10/042,865
CURRENT APPLICATION NUMBER: G0/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: G0/272,338
PRIOR FILING DATE: 2001-01-09
PRIOR PLING DATE: 2001-03-09
PRIOR PLING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-03
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TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHANNEL
TITLE OF INVENTION: ACTIVATING PROTEASE 1 (CAPI) GENE DISRUPTIONS
FILE REFERENCE: R-490
CURRENT APPLICATION NUMBER: US/10/109,616
CURRENT APPLICATION NUMBER: US 60/280,509
FRIOR FILING DATE: 2001-03-29
FRIOR FILING DATE: 2001-03-29
FRIOR FILING DATE: 2001-03-8
FRIOR FILING DATE: 301-03-8
FRIOR FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 73.6%; Score 39; DB 12; Length 339; Best Local Similarity 75.0%; Pred. No. 1.2e+02; Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-10-109-616-2
i, Sequence 2, Application US/10109616
i, Publication No. US20030167484A1
i, GENERAL INFORMATION:
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CORGANISM: Mus musculus
US-10-042-865-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 PRITGGGS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 PRITGGGS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PRVTGGGA 9
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Matches 6: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-109-616-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
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RESULT 12 US-10-042-865-151

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APPLICANT: Gerlach, Valerie L.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Millet, Isabelle
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Stone, Using the Same
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE KEFEKENCE: 1.140.7-53,
CURRENT PEDELICATION NUMBER: US/10/042,865
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR PILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-0
PRIOR FILING DATE: 2001-01-0
PRIOR FILING DATE: 2001-01-0
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-18
NUMBER OF SEQ ID NOS: 264
SOFTWARE: PAECHLIN VET. 2.1
ENGTH: 342
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Application US/10042865
5. US20040029216A1
                                                                                                                                                                                                                              Zhong, Mei
Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
                                                                                                                                                                                                                                                                                                                                                                                Tchernev, Velizar T
Miller, Charles E
Guo, Xiaojia
Boldog, Ference L
Grosse, Milliam M
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APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan D
APPLICANT: Casman, Stacie J
                                                                          APPLICANT: Padigaru, Muralidhara
                                                                                                            Li, Li
Zerhusen, Bryan D
                                                                                                                                                      Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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  Sequence 151, Applica
Publication No. US200
GENERAL INFORMATION:
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US-10-042-865-15:
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APPLICANT: BURGES, Catherine E

TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
TITLE OF INVENTION: URSING THE SAME
FILE REFERENCE: 21402-245
CURRENT APPLICATION NUMBER: US/10/051,874
CURRENT PILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: 60/268,595
PRIOR APPLICATION NUMBER: 60/262,587
PRIOR APPLICATION NUMBER: 60/262,587
PRIOR APPLICATION NUMBER: 60/262,454
PRIOR APPLICATION NUMBER: 60/272,409
PRIOR APPLICATION NUMBER: 60/276,777
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-31
PRIOR PELING DATE: 2001-03-46
PRIOR PELING DATE: 2001-03-46
PRIOR PELING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/236,336
PRIOR PELING DATE: 2001-10-18
PRIOR PELING DATE: 2001-10-13
PRIOR APPLICATION NUMBER: 60/265,530
PRIOR PELING DATE: 2001-01-31
PRIOR PELING DATE: 2001-01-31
PRIOR PELING DATE: 2001-01-31
PRIOR PELING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 269
NUMBER OF SEQ ID NOS: 269
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Publication No. US20040029216A1
GENERAL INFORMATION:
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Grosse, William M
Alsobrook II, John P
Gerlach, Valerie L
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Gangolli, Esha A
Burgess, Catherine E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Padigaru, Muralidhara
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Miller, Charles E
Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li, Li
Zerhusen, Bryan D
Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
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                                             Rothenberg, Mark
Stone, David J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.0%
....hes 6; Conservative
                    Ellerman, Karen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 PRITGGGS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PRVTGGGA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-042-865-153
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LENGTH: 285
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Variant human cytomegalovirus peptide epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Prea. ... o; Mismatches
CURRENT FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: US/09/692,170C
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 09/534,639
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 1000-03-27
PRIOR FILING DATE: 1998-05-11
PRIOR FILING DATE: 1998-05-10
PRIOR FILING DATE: 1998-02-10
PRIOR FILING DATE: 1998-02-10
PRIOR PLING DATE: 1998-02-10
PRIOR PLING DATE: 1998-01-14
PRIOR PLING DATE: 1999-10-14
PRIOR PLING DATE: 1997-10-14
PRIOR PLING DATE: 1997-10-14
PRIOR FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (10)...(10)
OTHER INFORMATION: Xaa = L, F or M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 89, Application US/10051874 Publication No. US20040005557A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Padigaru, Muralidhara
APPLICANT: Alsobrook II, John P
APPLICANT: Colman, Steven D
APPLICANT: Spytek, Kimberly A
APPLICANT: Boldog, Ferenc
APPLICANT: Vernet, Corine AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patturajan, Meera
Shimkete, Richard A
Pena, Carol EA
Tchernev, Velizar T
Zerhusen, Bryan D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baumgartner, Jason C
Herrman, John L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li, Li
Shenoy, Suresh G
Casman, Stacie J
Guo, Xiaojia Sasha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Edinger, Shlomit R
MacDougall, John R
Malyankar, Uriel M
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerlach, Valerie
Grosse, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Willet, Isabelle
Miller, Charles E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lepley, Denise M
Smithson, Glennda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peyman, John A
Gorman, Linda
Mezes, Peter D
Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC_FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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APPLICANT: Diamond, Don J.
TILLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS
FILE REFERENCE: 1954-346
CURRENT APPLICATION NUMBER: US/10/405,231
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CURRENT APPLICATION NUMBER: US/10/238,607
CURRENT FILING DATE: 2002-12-09
PRIOR PELING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 09/534,639
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 1000-03-27
PRIOR FILING DATE: 1938-05-11
PRIOR FILING DATE: 1938-05-11
PRIOR PILING DATE: 1938-02-10
PRIOR PLING DATE: 1938-02-10
PRIOR PLING DATE: 1938-02-10
PRIOR PLING DATE: 1938-01-14
PRIOR PLING DATE: 1938-01-14
PRIOR APPLICATION NUMBER: US 08/950,064
PRIOR APPLICATION NUMBER: US 08/950,064
PRIOR APPLICATION NUMBER: US 08/950,064
PRIOR PILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VETSION 3.1
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48; DB 14; Length 10;
Pred. No. 0.11;
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                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-223-538-8
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DCATION: (10)..(10)

CTHER INFORMATION: Xaa = L, F or M

US-10-238-607-8
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; Sequence 8, Application US/10405231
; Publication No. US20030190328A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 8, Application US/10238607; Publication No. US20030118602A1; GENERAL INFORMATION:
                                                                         LENGTH: 579 amino acids
TYPE: amino acid
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial sequence
                   INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                   407 TPRVTGGGAM 416
                                                                                                                                                                                                                                                                                                                                                               1 TPRVTGGGAM 10
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Kari, Csaba
TITLE OF INVENTION: No. US20030120060Alel Cytomegalovirus DNA Constructs and
Uses Therefor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 10; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: The Wistar Institute of, Anatomy & Biology Gonczol, Eva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/223,538
FILING DATE: 19-Aug-2002
CLASSIFICATION NUMBER: US/09/11,699
FILING DATE: 19-Aug-2002
CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/09/11,699
FILING DATE: 19-Jan-1999
APPLICATION NUMBER: US 60/015,717
FILING DATE: 23-APR-1996
ATTORNEY/AGENT INFORMATION:

NAME: Kodroff, Cathy A.

REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: WST66APCT
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/171,699
PILING DATE: 19-Jan-1999
APPLICATION NUMBER: US 60/015,717
FILING DATE: 23-APR-196
ATTORNEY/AGENT INFORMATION:
NAME: KOdroff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: 33,780
TELECOMMUNICATION INFORMATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/223,538
FILING DATE: 19-AUG-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-223-538-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/10223538; Publication No. US20030120060A1
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 561 TYPE: PRT
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STATE: Pennsylvania
COUNTRY: USA
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ORGANISM: Homo sapiens
                                                                                                                                                       ORGANISM: Homo sapiens
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US-09-812-079A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-434-982-2
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Sequence 7, Application US/10465231

Publication No. US20030190328A1

GENERAL INFORMATION:

APPLICATION

TITLE OF INVENTION: INMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS

FILE REFERENCE: 1954-346

CURRENT PILING DATE: 2003-04-03

PRIOR APPLICATION NUMBER: US/09/692,170C

PRIOR APPLICATION NUMBER: US 09/534,639

PRIOR PILING DATE: 2000-03-27

PRIOR PILING DATE: 1998-05-11

PRIOR PILING DATE: 1998-05-11

PRIOR PILING DATE: 1998-05-11

PRIOR PILING DATE: 1998-01-04

PRIOR PILING DATE: 1998-01-14

PRIOR PILING DATE: 1998-01-14

PRIOR PILING DATE: 1997-10-14

PRIOR PILING DATE: 1997-10-14
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                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 53; DB 14; Length 10; Best Local Similarity 100.0%; Pred. No. 0.016; Matches 10; Conservative 0; Mismatches 0; Indels
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Patent No. US20020058038A1
GENERAL INFORMATION:
TITLE OF INVENTION: THERAPEUTIC ANTI-CYTOMEGALOVIRUS
TITLE OF INVENTION: THERAPEUTIC ANTI-CYTOMEGALOVIRUS
TITLE OF INVENTION: COMPOUNDS
TITLE REPREMENTS 209500
CURRENT APPLICATION NUMBER: US/09/812,079A
CURRENT APPLICATION NUMBER: 60/191,050
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                             TYPE: PRT ORGANISM: Human cytomegalovirus
           PRIOR FILING DATE: 1996-11-12
NUMBER OF SEQ ID NOS: 43
SOFFWARE: Patentin version 3.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                               LENGIH: 10
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Gonczol, Eva
Berencsi, Klara
Kari, Caba
TITLE OF INVENTION: No. US20030120060Alel Cytomegalovirus DNA Constructs and
Uses Therefor
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Sequence 2, Application US/10434982

Publication No. US20030199673A1

GENERAL INFORMATION:

APPLICANT: Nicolette, Charles A.

TITLE OF INVENTION: THERAPEUTIC ANTI-CYTOMEGALOVIRUS COMPOUNDS

FILE REPRENKE: SO 108C

CURRENT APPLICATION NUMBER: US/10/434,982

PRIOR PILING DATE: 2003-05-10

PRIOR PLILING DATE: 2000-03-1

PRIOR PLILING DATE: 2000-03-1

PRIOR PLILING DATE: 2000-03-21

PRIOR PLILING DATE: 2000-03-21

PRIOR PLILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin version 3.1
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Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 10; Conservative 0; Mismatches 0; Indels (
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Query Match
100.0%; Score 53; DB 9; Length 561;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gequence 6, Application US/10223538
publication No. US20030120060A1
general INFORMATION:
APPLICANT: The Wistar Institute of, Anatomy & Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
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equence 432, equen	Sequence 132, App Sequence 132, App Sequence 432, App Sequence 432	THEREFOR
346 14 US-1 346 14 US-1	14 08-11 14 08-11	RESULT 1 US-10-238-607-7 Sequence 7, Application US/10238607 Sequence 7, Application US/10238607 Sequence 7, Application US/10238607 GENERAL INFORMATION: TITLE OF INVENTION: HCMV- REACTIVE T CELLS AND USES TITLE OF INVENTION HCMV- REACTIVE T CELLS AND USES CURRENT FILING DATE: 1954-398 CURRENT FAPPLICATION NUMBER: US/10/238,607 CURRENT FILING DATE: 2002-12-09 PRIOR PILING DATE: 2000-10-20 PRIOR PAPLICATION NUMBER: US 09/692,170 PRIOR FILING DATE: 1998-05-11 PRIOR FILING DATE: 1998-05-11 PRIOR FILING DATE: 1998-05-10 PRIOR FILING DATE: 1998-05-10 PRIOR FILING DATE: 1998-02-10 PRIOR PILING DATE: 1998-02-10
	7.47-7-7-7-7-7-7-7-7-7-7-7-7-7-7-7-7-7-7	RESULT 1 US-10-218-607-7 Sequence 7, Appl; Publication No. () GENERAL INCORATION TITLE OF INVENTY TITLE OF INVENTY FILE REPERBICE: CURRENT APPLICATION PRIOR PAPLICATION PRIOR PLING DAN PRIOR PLING DAN PRIOR PLING DAN PRIOR FILING DAN PRIOR APPLICATION PRIOR FILING DAN PRIOR PAPLICATION
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March 18, 2004, 00:55:18; Search time 39 Seconds (without alignments) 66.009 Million cell updates/sec Run on:

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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1045404 seqs, 257433775 residues Searched: 1045404 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 7, Appli	Sequence 7, Appli	Sequence 2, Appli		Sequence 6, Appli		Sequence 8, Appli	ω,	89,	Sequence 153, App	Sequence 2, Appli	Sequence 151, App	152,	Sequence 154, App	86, A	
SUMMARIES	Ω	US-10-238-607-7	US-10-405-231-7	US-09-812-079A-2	US-10-434-982-2	US-10-223-538-6	US-10-223-538-8	US-10-238-607-8	US-10-405-231-8	US-10-051-874-89	US-10-042-865-153	US-10-109-616-2	US-10-042-865-151	US-10-042-865-152	US-10-042-865-154	US-10-051-874-86	
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C;Accession: J01252
R;Levay, K.; Zavriev, S.
B;Levay, K.; Zavriev, S.
J;Gen. Virol. 72, 2333-2337, 1991
A;Title: Vuclectide sequence and gene organization of the 3'-terminal region of chrysant A;Reference number: J01246; MUID:92013948; PMID:1919520
A;Accession: J01252
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C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Species: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession. AD3294
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
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A;Modecule type: DNA
A;Residues: .1-180 cKUR>
A;Cross-references: GB:AE008917; PIDN:AAL51519.1; PID:g17982235; GSPDB:GN00190
A;Experimental source: strain 16M
hypothetical 16.7K protein - chrysanthemum virus B
C;Species: chrysanthemum virus B
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
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                                                                                                                                                                                                                                                                                                                                                A;Molecule type: genomic RNA A;Residues: 1-164 <LEV>
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54 SPRILGGG 61
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Gaps

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Gaps .; 0

62.3%; Score 33; DB 2; Length 180; 75.0%; Pred. No. 1.1e+02; Live 0; Mismatches 2; Indels

Best Local Similarity 75.03 Matches 6; Conservative

Query Match

Search completed: March 7, 2004, 13:02:55 Job time : 36 secs

127 TPEVTSGG 134

1 TPRVTGGG 8

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RESULT 44

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S55017
hypochetical protein 2 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 16-Feb-1997
C;Accession: S55017
E;Bergstrom, D.E.; Merli, C.A.; Cygan, J.A.; Shelby, R.; Blackman, R.K.
Genetics 139, 1331-1346, 1995
A;Title: Regulatory autonomy and molecular characterization of the Drosophila out at first A;Reference number: S55016; MUID:95286060; PMID:7768442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T36374
F;Olivar, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
A;Accession: T36374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-147 <OLL>
A;Cross-references: EMBL:AL049628; PIDN:CAB40863.1; GSPDB:GN00070; SCOEDB:SCE94.14
A;Experimental source: strain A3(2)
C;Genetics:
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
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                                                                                                                                                                                                     A;Residues: 1-125 <STO>
A;Cross-references: GB:AE002093; NID:g4417270; PIDN:AAD20395.1; GSPDB:GN00139
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A;Gene. R-2221750
A;Map position: 2
C;Superfamily: Arabidopsis thaliana hypothetical protein T22F8.240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 62.3%; Score 33; DB 2; Length 125; Best Local Similarity 75.0%; Pred. No. 76; Matches 6; Conservative 1; Mismatches 1; Indels
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A,Molecule type: DNA
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Pred. No. 93;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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Best Local Similarity 66.7%;
Matches 6; Conservative
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nes 6; Conserv
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A; Residues: 1-154 <BER>
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A;Gene: FlyBase:oaf
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J. Biochem. 115, 608-614, 1994
J. Biochem. 115, 608-614, 1994
J. Richem. 115, 608-614, 1994
J. Reference number: JC2269; MUID:94334310; PMID:7520038
J. Reference number: MID:94334310; PMID:7520038
J. Reference mumber: MID:9434310; PMID:7520038
J. Residues: 1-113 «KUR»
J. Residues: 1-113 «KUR»
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C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C;Accession: JC2270; PC2187
                                                                                                                                                                                                                                                                                                                               C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
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A;Residues: 1-21 «KU2>
A;Reperimental source: hybridoma cell
C;Comment: This protein is specific to human P-selectin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-101/Region: V segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: mRNA
A,Residues: 1-111 <RUF>
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heteroterramer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <IMM>
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Pred. No. 68;
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                                                                                                                                                                                                                                                    Ig kappa chain V region (Py42) - mouse C;Species: Mus musculus (house mouse)
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75.0%;
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Best Local Similarity 75.v.
Frag 6; Conservative
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97 TPRTFGGG 104
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RESULT 46

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Ig kappa chain V region (2GB) - mouse
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Accession: B37266
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti-A;Reference number: A38740; MuID:91177923; PMID:1706720
                                                                                                                                                                                                                                                                                                            A;Residues: 1-3300 <COL>
A;Cross-references: GB:295324; GB:AL123456; NID:g3261760; PIDN:CAB08587.1; PID:e1299834;
A;Experimental source: strain H37Rv
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authories: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUD:98295987; PMID:9634230
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C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
Modecule type: mRNA
A;Residues: 1-23 <PLA>
A;Cross_references: EMBL:X71026; NID:g506575; PIDN:CAA50343.1; PID:g510308
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C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
F; 19-93/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: T-cell receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: $47208
K; Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.
submitted to the EMBL Data Library, February 1993
A; Reference number: $40133
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Best Local Similarity 66./*,
-hea 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 PRVTGGGAM 10
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Best Local Similarity
6; Conserve
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Best Local Similarity
Matchés 6; Conserva
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                                                                                                                                                                                                                                                                                                                     A38149
RNA-directed RNA polymerase (EC 2.7.7.48) - yeast (Saccharomyces cerevisiae) RNA replicd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: T51890
S;Schulte, U.; Algn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, August 2000
A;Reference number: Z25858
                                                                                                                                                                                                                                                                                                                                                         C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
B;Bateban, L.M.; Rodriguez-Cousino, N.; Esteban, R.
J. Biol. Chem. 267, 10874-10881, 1992
J. Biol. Chem. 267, 10874-10881, 1992
A;Title: T double-stranded RNA (deRNA) sequence reveals that T and W deRNAs form a new FARcession: A38149; MUID:92268145; PMID:1587863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: D70575
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
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A;Residues: 1-940 coFFs.
A;Cross-references: EMBL:W06595; NID:g4079660; PIDN:AAC98708.1; PID:g4079661
A;Cross-sequence extracted from NCBI backbone (NCBIN:103899, NCBIP:103891)
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C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
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A;Cross-references: EMBL:AL391572; GSPDB:GN00116; NCSP:B23111.20
A;Experimental source: BAC clone B23111; strain OR74A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 64.2%; Score 34; DB 2; Length 940; Best Local Similarity 66.7%; Pred. No. 3.6e+02; Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                   2; Indels
                                                        66.7%; Pred. No. 1.7e+02;
                                                                                      Mismatches
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                                                                                   Conservative
                                                                                                                                                                                                 126 PKVDGGGPM 134
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                                                                                                                                           2 PRVTGGGAM 10
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                                                     Best Local Similarity
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Matches
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Circlession: G96600
RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 40B, 816-820, 2000
Aputhors: Hunter, J.L.; Johnison-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I Arxides: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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R;She, Q; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-V Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-V Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-408 <COL>
A.Cross-references: GB:Z74024; GB:AL123456; NID:g3250700; PIDN:CAA98377.1; PID:e1301025;
A.Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE006641; NID:g13816397; PIDN:AAK43110.1; GSPDB:GN00155
C;Genetics:
A;Gene: SSO3008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dehydrogenase, probable [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May_2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                    64.2%; Score 34; DB 2; Length 408; 60.0%; Pred. No. 1.6e+02; Live 2; Mismatches 2; Indels
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Pred. No. 1.6e+02;
3; Mismatches 1; Indels
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55.6%;
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Best Local Similarity 60.0.
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Best Local Similarity 55.0.
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A; Residues: 1-409 < KUR>
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A; Status: preliminary
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A;Map position: 1
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                                     C; Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001 C; Accession: F95101
R; Tettelin, H.; Nelson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A; Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: G70225
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Deltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Hamlin, R.; Holroyd, S. Mature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:99295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-380 <KUR>
A;Residues: GB:AE005672; PIDN:AAK75007.1; PID:g14972353; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 183, 5709-5717, 2001
A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A; Jitle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A; Reference number: A97872; MUID:21429245; PMID:11544234
A; Accession: G97869
A; Status: preliminary
A; Molecule type: DNA
A; Residuals: 1-380 <KUR>
A; Cross-references: GB: AE007317; PIDN: AAK99587.1; PID:g15458380; GSPDB:GN00174
C; Genetics:
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C;Species: Streptococcus pneumoniae
C;Date: 2-2-0ct-2001 #sequence_revision 22-0ct-2001 #text_change 02-Nov-2001
C;Accession: G97969
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.;
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.;
Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
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Pred. No. 1.5e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 380;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.2%; Score 34; DB 2; L
75.0%; Pred. No. 1.5e+02;
live 1; Mismatches 1;
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C,Superfamily: nitrogen fixation protein nifS
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75.0%;
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Best Local Similarity 75.0°,
-hag 6; Conservative
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Matches 6; Conserv
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A,Status: preliminary
A,Molecule type: DNA
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A;Accession: JA0131
A;Molecule type: genomic RNA
A;Rotesidues: 1-380 «ROC>
A;Cross-references: GB:MZ5270; NID:g323338; PIDN:AAA42904.1; PID:g323341
A;Cross-references: GB:MZ5270; NID:g323338; PIDN:AAA42904.1; PID:g323341
C;Comment: The genome is a single-stranded, positive-sense RNA. It codes for 33K, 92K, 4(
are core proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rigoodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title; Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein AGR_C_764 [imported] - Agrobacterium tumefaciens (strain C58, Cereor C,Species: Agrobacterium tumefaciens
C,Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1.370 «KUR»
A;Cross-references: GB:AE007869; PIDN:AAK86246.1; PID:g15155352; GSPDB:GN00169
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R,Rochon, D.M.; Tremaine, J.H.
Virology 169, 251-259, 1989
A;Title: Complete nucleotide sequence of the cucumber necrosis virus genome.
A;Reference number: A94391; MUID:89204896; PMID:2705296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: host Cucumis sativus (cucumber)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-Jul-1999
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                                                      Query Match 64.2%; Score 34; DB 2; Length 370; Best Local Similarity 85.7%; Pred. No. 1.46+02; Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 64.2%; Score 34; DB 2; Length 370; Best Local Similarity 85.7%; Pred. No. 1.4e+02; Matches 6; Conservative 0; Mismatches 1; Indels
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A;Gene: AGR C 764
A;Map position: circular chromosome
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   A; Map position: circular chromosome
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Matches 5; Conservative
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TPSISGGGTI 327
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Fitle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE001965; GB:AE000513; NID:g6458892; PIDN:AAF10733.1; PID:g645889
A;Experimental source: strain Rl
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A, Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A, Reference number: AB2577; MUID:21608550; PMID:11743193
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A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uricase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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64.2%; Score 34; DB 2; Length 288; Best Local Similarity 55.6%; Pred. No. 1.1e+02; Matches 5; Conservative 3; Mismatches 1; Indels
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Pred. No. 1.2e+02;
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                                                                                                                                           A Map position: 4
A;Introns: 57/3; 96/3; 153/3; 224/3
A;Note: F2009.200
C;Superfamily: erythrocyte band 7 integral membrane protein
A;Molecule type: DNA
A;Residues: 1-288 <BEV>
A;Cross-references: EMBL:AL021749
A;Experimental source: cultivar Columbia; BAC clone F2009
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87.5%;
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Best Local Similarity 87.55
Matches 7; Conservative
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7 PKIPGGGAI 15
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A;Gene: dcd
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RESULT 25

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prohibitin-like protein F2009.200 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 19-May-2000
C;Accession: T04622
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X. submitted to the Protein Sequence Database, October 1998
                                                    Cjaccession: AE1114

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquerc, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ridaer, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat A; C.; Schlueer, T.; Sinnees, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; WUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hydroxyethylthiazole kinase (ThiM) homolog lin0341 [imported] - Listeria innocua (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: lin0341
C;Superfamily: hydroxyethylthiazole kinase; hydroxyethylthiazole kinase homology
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A,MoLecule type: DNA
A,Residues: 1.269 < GLA>
A,Residues: GB:AL592022; PIDN:CAC95574.1; PID:g16412770; GSPDB:GN00178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AF1475
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
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55.6%; Pred. No. 1.18+02;
1.10dels
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55.6%;
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Best Local Similarity 55.6'
Matches 5; Conservative
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les 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                        A, Molecule type: DNA
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:111016950
A;Accession: A84233
                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein BH1384 [imported] - Bacillus halodurans (strain C-125) C; Species: Bacillus halodurans C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C; Accession: H838co. K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 Nucleic Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MuID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB05103.1; GSPDB:GN0d
A;Experimental source: strain C-125
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                                                                                          Length 247;
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                                                                                                                                                     1; Indels
                                                                                             DB 2;
                                                                                       Score 34; DB 2; Pred. No. 97; 1; Mismatches
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Pred. No. 99;
2; Mismatches
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                                                                                                                      75.0%;
      A;Cross-references: SGD:S003029
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Best Local Similarity 66.7-
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les 6; Conservative
                                                                                                                      Best Local Similarity 75.0 Matches 6; Conservative
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A;Molecule type: DNA
A;Residues: 1-267 <STO>
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A; Residues: 1-252 <STO>
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                                     A; Map position: 7L
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A;Gene: BH1384
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RESULT 27

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A,Status: preliminary; translated from GB/EMBL/DDBJ.
A,Status: preliminary; translated from GB/EMBL/DDBJ.
A,Status: preliminary; translated from GB/EMBL/DDBJ.
A,Molecule type: DNA
A,Rosidues: 1-3643 s.SAU-
A,Cross-references: EMBL:AL109974; PIDN:CAB53322.1; GSPDB:GN00070; SCOEDB:SCF34.11c
A;Genetics:
C,Genetics: SCOEDB:SCF34.11c
A;Genetics: protein; phosphopantetheine; phosphoprotein
F;GSTODmain: actate-CoA ligase homology (ACL1-
F;GTODmain: actate-CoA ligase homology (ACL2-
F;140-2207/Domain: actate-CoA ligase homology (ACL2-
F;1101-3550/Domain: actate-CoA ligase homology (ACL3-
F;1101-350/Domain: actate-CoA ligase homology (ACR3-
F;1101-350/Domain: actate-CoA ligase homology (ACR3-)
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A;Residues: 1-247 <PEU>
A;Cross-references: EMBL:Z72583; NID:g1322563; PID:e243286; PID:g1322564; GSPDB:GN00007;
A;Experimental source: strain S288C
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R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
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N;Alternate names: hypothetical protein G3432
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C;Accession: $64065
R;Feuramann, M: Potier, S.; Souciet, J.L.
R;Feuramann, M: Potier, S.; Souciet, J.L.
A;Reference number: $64044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
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A,Experimental source: BAC clone B8B20; strain OR74A
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A,Map position: 6
C,Superfamily: Neurospora crassa hypothetical protein B8B20.250
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nes 6; Conservative
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A;Accession: T49671
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-211 <SCH>
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R;Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, September 1999
A;Reference number: Z21606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Accession: E70820
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Natlandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Natures 393, 537-544, 1998
A,Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A,Reference number: A70500; MuID:98295987; FMID:9634230
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A.Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: EMBL:Z50046; NID:g899393; PIDN:CAA90368.1; PID:g899395; MIPS:YDR145w
A,Experimental source: strain AB972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical glycine-rich protein Rv0977 - Mycobacterium tuberculosis (strain H37RV)
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A;Molecule type: DNA
A;Residues: 1-923 <COL>
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C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                      hypothetical protein YDR145w - yeast (Saccharomyces cerevisiae)
N;Alernate names: hypothetical protein YD8358.02
C;Species: Saccharomyces cerevisiae
C;Species: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 29-Oct-1999
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A)Cross-references: SGD:S0002552; MIPS:YDR145w
A;Map position: 4R
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       470 PRVSGGG 476
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Chin, C.W.; Chung, M.K.; Conn, L.; Corway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 166-820, 2000
Nature 408, 166-820, 2000
Nature 408, 168-820, 2000
Nature 408, 167-820, 2000
Nature 508, 167-820, 200
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A; Introns: 19/1; 89/1; 183/3; 239/2; 364/3; 394/1; 447/2
C; Superfamily: glucosylceramidase
C; Keywords: glycoprotein; glycosidase; hydrolase; lysosome; membrane bound; sphingolipid
F; 1-21, Domain: signal sequence #status predicted <SIG>
F; 22-522/Product: glucosylceramidase #status predicted <MPT>
F; 42,86,90,274,428/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Molecule type: DNA
A;Residues: 1-522 <MI2>
A;Cross-references: EMBL:281058; PIDN:CAB02924.1; GSPDB:GN00022; CESP:F11E6.1
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H86228
                                                   C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C,Accession: T18583; T20789
                       glucosylceramidase (EC 3.2.1.45) precursor - Caenorhabditis elegans
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A;Molecule type: DNA
A;Residues: 1-522 <WIL>
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submitted to the EMBL Data Library, October 1996
A;Reference number: 219324
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                                                                                                                                                                                                                submitted to the EMBL Data Library, August 1998
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Matches 6; Conservative
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Matches 7; Conservative
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A;Accession: T18583
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C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: JC7280
R;Hiroyama, T.; Iwama, A.; Morita, Y.; Nakamura, Y.; Shibuya, A.; Nakauchi, H.
Biochem. Biophys. Res. Commun. 272, 224-229, 2000
A;Title: Molecular cloning and characterization of CRLM-2, a novel type I cytokine recepta Reference number: JC7280
A;Contents: Embryo
A;Accession: JC7280
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R;Del Sal, G.; Collavin, L.; Ruaro, M.E.; Edomi, P.; Saccone, S.; della Valle, G.; Schne Proc. Natl. Acad. Sci. U.S.A. 91, 1848-1852, 1994
A;Title: Structure, function, and chromosome mapping of the growth-suppressing human hom A;Reference number: A53138; MUID:94173926; PMID:8127893
A;Accession: A53138
A;Status: preliminary; translated from GB/EMBL/DDBJ
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-336 <ARN>
A/Cross-references: GB.AE001800; GB:AE000512; NID:g4982090; PIDN:AAD36611.1; PID:g498211
A/Experimental source: strain MSB8
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
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A;Cross-references: GB:L13698; NID:g472859; PIDN:AAA72368.1; PID:g472860
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                                                                                                                                                                                                                                                                                                                                                                         66.0%; Score 35; DB 2; Length 336; 75.0%; Pred. No. 86; tive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                      C.Superfamily: rod shape-determining protein envB
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Pred. No.
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 77.8'
----- 7; Conservative
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Matches 6; Conservative
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148 PRTSGGGA 155
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280 RLTGGGAL 287
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les 6; Conserv
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A; Residues: 1-359 < HIR>
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Mypothetical protein AGR C_4682 [imported] - Agrobacterium tumefaciens (strain C58, Cerec Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C; Accession: C97669 B; A: Hinkle, G., Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A: Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001 A; A: Liu, F.; Mollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A; Hitle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A; Reference number: A97359; MUID:21608551; PMID:11743194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq. A;Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                             R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelle f. Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
      conserved hypothetical protein Atu2585 [imported] - Agrobacterium tumefaciens (strain C56
C,Species: Agrobacterium tumefaciens
C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                      ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-223 «KUR»
A; Cross-references: GB: AE008688; PIDN: AAL43566.1; PID: 917741080; GSPDB: GN00186
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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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A;Map position: circular chromosome
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Best Local Similarity 70.0.
To 7; Conservative
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Best Local Similarity 70...
7, Conservative
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                                                                                                                     C; Accession: AH2893
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C;Superfamily: 1,4-alpha-glucan branching enzyme
C;Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                           1,4-alpha-glucan branching enzyme (EC 2.4.1.18) IIb - maize
N.Alternate names: starch branching enzyme IIb
C;Species: Zea mays (maize)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 18-Jun-1999
C;Accession: T01663
R;Kim, K.N.; Fisher, D.K.; Gao, M.; Guiltinan, M.J.
Sibmitted to the EMBL Data Library, June 1998
A,Description: Molecular cloning and characterization of the amylose-extender gene encod A;Reference number: Z14387
A,Accession: T01663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 38/1; 86/3; 138/2; 171/2; 185/3; 205/3; 232/3; 271/3; 299/3; 340/2; 380/2; 44
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C;Superfamily: 1,4-alpha-glucan branching enzyme
C;Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase
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A;Experimental source: strain B73
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C;Dacte: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 18-Jun-1999
C;Accession: T02981
R;Fisher, D.K.; Boyer, C.D.; Hannah, L.C.
Plant Physiol. 102, 1045-1046, 1993
A;Title: Starch branching enzyme II from maize endosperm.
A;Reference number: Z14808; MUID:94105320; PMID:8278524
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A;Residues: 1-799 <-FIS>
A;Cross-references: RMBL:LO8065; NID:g168482; PIDN:AAA18571.1; PID:g168483
A;Experimental source: cultivar W64AX182E
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85.7%; Pred. No. 1.3e+02;
tive 1; Mismatches 0; Indels
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A;Molecule type: DNA
A;Residues: 1-799 <KIM>
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Best Local Similarity 85.74
E. Conservative
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134 RITGGGAI 141
3 RVTGGGAM 10
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A;Residues: 1.788 <AQF>
A;Coss.references: GB:AE000748; NID:g2983960; PIDN:AAC07512.1; PID:g2983965; GB:AE000657; A;Cross.references: GB:AE000748; NID:g2983960; PIDN:AAC07512.1; PID:g2983965; GB:AE000657; GGenetics: A;Genetics: A;Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Vysotskaia, V.S.; Schwartz, J.R.; Kwan, A.; Toriumi, M.; Yu, G.; Oji, O.; Liu, S.; Li, rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N. submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome 1 BAC T13D8 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A,Reference number: A70300; MUID:98196666; PMID:9537320
A,Accession: C70441
                                                                                                                                                                                                                                                              A; Cross-references: EMBL: AL023496; NID: e1292348; PID: e1292360; PIDN: CAA18910.1
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: C70441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T13D8.31 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 10-Dec-1999
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A;Introns: 15/1; 70/1; 90/2; 145/3; 185/3; 217/2; 248/3; 292/3; 330/2
A;Note: T13D8.31
C;Superfamily: Saccharomyces hypothetical protein YDR531w
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Pred. No. 65;
2; Mismatches 0; Indels
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A;Residues: 1-404 <VYS>
A;Cross-references: EMBL:AC004473; NID:G3108025; PID:G3249085
R.Parkhill, J.; Bentley, S.D.; Barrell, B.G.; Rajandream, M.A.submitted to the EMBL Data Library, January 1999
A;Reference number: Z20512
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A;Molecule type: DNA
A;Residues: 1-388 <PAR>
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Best Local Similarity 75.0%;
Matches 6; Conservative
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hes 6; Conserv
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A; Cross-references: BMBL: M74162; NID: 9146213; PIDN: AAA23909.1; PID: 9146214
A; Cross-references: BMBL: M74162; NID: 9146213; PIDN: AAA23909.1; PID: 9146214
F; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID: 97426617; PMID: 9278503
                                                glfF protein precursor - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: S25281; H6512
R;Castano, I.; Flores, N.; Valle, F.; Covarrubias, A.A.; Bolivar, F.
R;Castano, I.; Flores, N.; Valle, F.; Covarrubias, A.A.; Bolivar, F.
A;Title: gltF, a member of the gltBDF operon of Escherichia coli, is involved in nitroge
A;Reference number: S25281; MUID:93078627; PMID:1447980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE000401; GB:U00096; NID:g1789607; PIDN:AAC76246.1; PID:g1789608;
A;Experimental source: strain K-12, substrain MG1655
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A;Molecule type: DNA
A;Residues: 1-254 <BLAT>
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C, Species: Streptomyces coelicolor
C, Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
_C, Accession: T28693
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Fj.125/Domain: signal sequence #status predicted <SIG>
F;27-254/Product: gltP protein #status predicted <MAT>
F;213-229/Domain: transmembrane #status predicted <TMM>
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2; Mismatches
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Best Local Similarity 75.0
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N;Alternate names: 65K tegument protein

RESULT 2

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A;Status: preliminary
A;Molecule type: DNA
A;Status: DNA
A;Status: DNA
A;Molecule type: DNA
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A;Molecule type: DNA
A;Cross-references: GB:AE006469; PIDN:AAK64994.1; PID:G14523421; GSPDB:GN00165
A;Cross-references: GB:AE006469; PIDN:AAK64994.1; PID:G14523421; GSPDB:GN00165
A;Cross-references: GB:AE006469; PIDN:AAK64994.1; PID:G14523421; GSPDB:GN00165
A;Galibert, F: Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Mann, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Muthors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A;Muthors: Kahn, D.; Kahn, M. Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.(A)
A;Mitle: The composite genome of the legame symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
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R; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse Aslaman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A; Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti A; Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                               C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: C87280
R;Niacman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.;
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolons
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proco. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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Pred. No. 71;
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Best Local Similarity 81.8%;
Matches 9; Conservative
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62 TPSVTGGG 69
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A,Molecule type: DNA
A,Residues: 1-653 <STO>
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A;Gene: CC0252
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                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 17-Feb-1994 #text_change 17-Feb-1994
C;Date: 31-Mar-1992 #sequence_revision 17-Feb-1994 #text_change 17-Feb-1994
C;Accession: A46342; A39149
B;Pande, H.; Lee, T.D.; Churchill, M.A.; Zaia, J.A.
Virology 178, 6-14, 1990
A;Feberence mumber: A46342; MUID:90357792; PMID:2167561
A;Accession: A46342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Molecule type: protein
A;Residues: 1-561 <PA1>
Fy Fande, H.; Campo, K.; Tanamachi, B.; Zaia, J.A.
Virology 182, 220-228, 1991
A;Title: Human cytomegalovirus strain Towne pp65 gene: nucleotide sequence and expressic
A;Reference number: A39149; MUID:91220654; PMID:1850902
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A, Cross-references: GB: M67443
A, Cross-references: GB: M67443
A, Note: the authors translated the codon AAT for residue 478 as Asp C: Superfamily: cytomegalovirus lower matrix phosphoprotein C; Superfamily: cytomegalovirus lower matrix phosphoprotein C; Keywords: matrix protein; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Pred. No. 28;
0; Mismatches 1; Indels
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Best Local Similarity 100. Matches 10; Conservative

Query Match

A; Molecule type: DNA A; Accession: A39149

417 TPRVTGGGAM 426

RESULT 3

1 TPRVTGGGAM 10

ò 셤 RESULT 6

71.7%; 87.5%;

Query Match Best Local Similarity 87.57 Secondary 7; Conservative

A, Gene: F1511.14 A, Map position: 1

C;Genetics:

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-383 <STO>

1 TPRVTGGG 8

C37855 B81009 B82031 S58394 A82031 A82033 A82034 A43588 A43588 A43588 A702415 E601545 T702415 E601545 T702415 E60156 A6061 A60	C818 AF829 AF829 C876 C876 C486 C486 AH25 AH25 AH25 B463 B463 B463 B463 B463 B463 B463 B463
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		S22412 C87646 AC0699 G86279 E84316 T22589		736923 786072 786072 780817 197135 190500 177172
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ALIGNMENTS

GEK lower matrix phosphoprotein - human cytomegalovirus (strain AD169)
N;Alternate names: protein UL83
C;Species: human cytomegalovirus, human herpesvirus 5
C;Species: human cytomegalovirus, human herpesvirus 5
C;Date: 31-Mar-1989 #S0947
C;Datesion: A26793; 809847
C;Accession: A26793; 809847
C;Accession: A26793; 809847
C;Accession: A26793; B: Klages, S:, Walla, B.; Albrecht, J.; Fleckenstein, B.; Tomlinson, P.; Barre 7, Virol. 61, 446-453, 1987
A;Pitle: Primary structure and transcription of the genes coding for the two virion phos; A;Peference number: A93028; MUID:87112940; PMID:3027374

A, Accession: A2793
A, Accession: A2793
A, Residues: 1-561 < RUE>
A, References GB. M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.; I.M.; Barrell, B.G.
Curr. Top. Miorobiol. Immunol. 154, 125-169, 1990
A; Accession: 809749; MulD: 90269039; PMID: 2161319
A; Accession: 809847
A; Reference number: S09749; MulD: 90269039; PMID: 2161319
A; Residues: 1-561 < CHE>
A; Rossidues: 1-561 < CHE>
A; Rossidues: 1-561 < CHE>
A; Rossidues: Liss sequence was submitted to the EMBL Data Library, December 1989
C; Genetics: A, Rossidues: A

A;Introns: 93/3 C;Superfamily: cytomegalovirus lower matrix phosphoprotein C;Keywords: matrix protein; phosphoprotein

Gaps . Query Match
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 10; Conservative 0; Mismatches 0; Indels

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pyruvate, orthophos DNA mismatch repai hypothetical prote pyruvate, phosphat DNA-directed DNA p alphaP integrin - hypothetical prote hypothetical prote protoporphyrin IX hypothetical prote translation initia probable nuclear a hypothetical prote sill life prote sill life prote sill life prote probable PPE prote probable PPE prote probable PPE prote	droxy acide receptor by protein (c) protein (c) protein (c) protein (c) protein (c) protein (c) protein (c) protein pr	<u> </u>
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AF0709 AF1527 H71815 CG3735 CG3735 CG3735 CG3735 CG3735 CG3735 AC1191 DN0441 DN0441 DN0441 DN0441 AC1549 AC1540 AC1646 AC2840 AC31144 AC31144 AC31144 AC31144 AC31144 AC31144 AC31144 AC311419 AC31144 AC31144 AC31144 AC31144 AC31144 AC31144 AC31144 AC31144 AC31144 AC31144 AC31144 AC31144 AC311413 AC31141413 AC31141413 AC31141414 AC311	11111111111111111111111111111111111111
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succinylglutamate lipoate-protein li lipoate-protein li lipoate-protein li conserved hypothet hypothetical protein li lipoate-protein li lipoate-protein li lipoate-protein li lipoate-protein li lipoate protein li mreB protein - Bac cell shape determin cell-shape determin rod shape-determin probable permease rod shape-determin rod shape-determin probable protein lipophypothetical protein regulator of ftsI hypothetical livision protein lipopolysaccharide transcription fact lipopolysaccharide transcription fact lipopolysaccharide

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176 31 58.5 274 2 H83525 177 31 58.5 275 1 E36516 178 31 58.5 289 2 S74632 178 31 58.5 289 2 S74632	31 58.5 296 2 31 58.5 296 2 31 58.5 298 2 31 58.5 299 2	31 58.5 311 2 31 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3	31 58.5 311 2	31 58.5 346 2 31 58.5 346 2 31 50 5 364 2	31 58.5 368 2	31 58.5 369 2	31 58.5 369 2 31 58.5 370 2	31 58.5 370 2 31 58.5 371 2	31 58.5 372 2	31 58.5 372 2 31 58.5 380 1	31 58.5 380 2	31 58.5 394 2 31 58.5 404 2	31 58.5 410 2	31 58.5 410 2 31 58.5 410 2	31 58.5 410 2	31 58.5 411 2 31 58.5 415 2	31 58.5 450 1	31 58.5 455 1 31 58.5 467 2	31 58.5 468 2 31 58.5 471 2	31 58.5 485 2	31 58.5 497 1	31 58.5 502 Z 31 58.5 515 2	31 58.5 530 2	31 58.5 530 2	31 58.5 534 2	31 58.5 542 2 31 58 5 546 2	31 58.5 549 2	31 58.5 549 2	31 58.5 602 2	, 31 58.5 612 2 31 58.5 614 2	31 58.5 625 2	31 58.5 648 1 31 58.5 650 2	31 58.5 678 2	31 58.5 696 2 31 58.5 696 2	31 58.5 707 2	31 58.5 768 2 31 58.5 805 1	31 58.5 821 2	31 58.5 844 2 F	31 58.5 847 1 31 58 5 883 2	31 58.5 894 2 6	31 58.5 904 2
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us-10-697-055-7.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 7, 2004, 13:01:12; Search time 20 Seconds (without alignments) 48.096 Million cell updates/sec

Title: Perfect score:

US-10-697-055-7 53 1 TPRVTGGGAM 10 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 500 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	65K lower matrix p	65K lower matrix p	hypothetical prote	penicillin-binding	hypothetical prote	gltF protein precu	probable lipoate p	hypothetical prote	hypothetical prote	lipoate-protein li	1,4-alpha-glucan b	1,4-alpha-glucan b	conserved hypothet	hypothetical prote	rod shape-determin	gas1 homolog - hum	cytokine receptor-		hypothetical prote		hypothetical glyci	>	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	hydroxyethylthiazo	hydroxyethylthiazo	prohibitin-like pr
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                                                                      Query Match 60.4%; Score 32; DB 1; Length 142; Best Local Similarity 100.0%; Pred. No. 53; Mismatches 6; Conservative 0; Mismatches 0; Indels
PT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
SQ SEQÜENCE 142 AA; 15756 MW; 5459FD6B08ERAE21 CRC64;
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3 RVTGGG 8 |||||| 67 RVTGGG 72

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Search completed: March 7, 2004, 13:03:18 Job time: 26 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOI. Biol. Cell 13:3646-3661(2002).
-!- FUNCTION: Essential for the proper formation of the cortical actin cytoskeleton. Involved in controlling the size of cortical patches perhaps by regulating the nucleation of filaments at the
                                                                                                                                                                                                                                       STRAIN=DDY 228;
MEDLINE=93328765; PubMed=8335689;
Holtzman D.A., Yang S., Drubin D.G.;
"Synthetic-lethal interactions identify two novel genes, SLA1 and
"Synthetic control membrane cytoskeleton assembly in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                             Delaveau T., Jacg C., Perea J.; "Sequence of a 12.7 kb segment of yeast chromosome II identifies a "Sequence of a 12.7 kb segment of persilike gene and several new open reading frames."; Yeast 8:761-768(1992).
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GO; GO:0005857; C:actin cortical patch (sensu Saccharomyces); IDA.

GO; GO:0008992; P:cytoskeletal protein binding; IMP.

GO; GO:0007015; P:actin filament organization; IMP.

GO; GO:0007047; P:cell wall organization and biogenesis; IMP.

GO; GO:0007121; P:polar budding; IMP.

InterPro; IPR001452; SH3.

InterPro; IPR007131; SHD1.
                                                                                                                                         Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22287476; PubMed=12388763; Dewar H., Warren D.T., Gardiner F.C., Gourlay C.G., Satish N., Dewar H., Andrews P.D., Ayscough K.R.; Richardson M.R., Andrews P.D., Ayscough K.R.; "Novel proteins linking the actin cytoskeleton to the endocytic machinery in Saccharomyces cerevisiae.";
                                                01-0CT-1993 (Rel. 27, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Cytoskeleton assembly control protein SLA1. SLA1 OR YBL007C OR YBL0321.
PRT; 1244 AA
                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: Interacts with LSB5.
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93070613; PubMed=1441753;
                                                                                                                                                                                                                                                                                                                                    cerevisiae.";
J. Cell Biol. 122:635-644(1993).
                                      (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, Z22810; CAA80463.1; -. EMBL, Z35768; CAA84826.1; -. EMBL, S47695, AAB23985.1; -. PIR; S2527; S25327. HSSP, Q03526; LAWJ.
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Pfam; PF03983; SHD1; 1.
PRINTS; PR00452; SH3DOMAIN.
PPCDOM; PD000066; SH3; 3.
SWART; SM00326; SH3; 3.
   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH LSB5.
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                    NCBI_TaxID=4932;
                                        01-OCT-1993
   SLA1 YEAST
                       P32790;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22482865; PubMed=12594514;
Langkjaer R.B., Cliften P.F., Johnston M., Piskur J.;
"Yeast genome duplication was followed by asynchronous differentiation
of duplicated genes.";
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces exiguus (Yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 421:848-852(2003).
-!- SIMILARITY: Belongs to the S9P family of ribosomal proteins.
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                                                   16 X 7 AA APPROXIMATE REPEATS OF
                                                                                                                                                                                                                                                                          62.3%; Score 33; DB 1; Length 1244; 66.7%; Pred. No. 3.1e+02; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                     1244 AA; 135848 MW; 7FD85AA776407624 CRC64;
         SH3 domain; Repeat.
SH3 1.
SH3 2.
SH3 3.
                                                                                                                                                                                                                                                                                                                                                                                                             0876B4; 0876B5;
10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10S ribosomal protein S16.
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          Cytoskeleton; Actin-binding;
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 SH3; 3
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PS50002;
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PRT; 1093 AA

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                       Peters J., Peters M., Lottspeich F., Schaefer W., Baumeister W.;
Peters J., Peters M., Lottspeich F., Schaefer W., Baumeister W.;
"Nucleotide sequence analysis of the gene encoding the Deinococcus
radiodurans surface protein, derived amino acid sequence, and
complementary protein chemical studies ";
J. Bacteriol. 169:5216-5223(1987)
-! FUNCTION: Shape maintenance, possible protection from noxious
-in Enzymes or exogenous and unsettling DNA, and may mediate homotypic
cell_cell contacts.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-
layer with hexagonal symmetry.

PTM: CONTAINS TIGHTLY BOUND REDUCING SUGARS (SIX PER POLYPEPTIDE
PTM: CONTAINS TIGHTLY BOUND REDUCING SUGARS (IN PER N-
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THE THE NATIONAL REGION THE HYDROPHILIC C-TERMINAL REGION RICH IN AROMATIC MISCELLANGEOUS: THE HYDROPHILIC C-TERMINAL REGION SERVE TO AND THE AS COULD BE ENGAGED IN INTERACTIONS WITH NUCLEIC ACIDS, AND THE BOUND FATTY ACIDS AND THE N-TERMINAL REGION COULD SERVE TO ANCHOR THE LAYER TO THE OUTER MEMBRANE OF D. RADIODURANS. HDI LAYER CONTAIN ABOUT 30% BETA STRUCTURE AND VIRTUALLY NO ALPHA HELIX.
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                                         01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Hexagonally packed intermediate-layer surface protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.3%; Score 33; DB 1; Length 1036; 60.0%; Pred. No. 2.6e+02; tive 1; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 RICH IN AROMATIC AA (29%).
108028 MW; AAFF98206A74AEEE CRC64;
                                                                                                                                                           Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
Deinococcaceae; Deinococcus.
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PROSITE; P800013; PROKAR LIPOPROTEIN; UNKNOWN 1.
Glycoprotein; Lipoprotein; Signal; Cell wall; S-layer.
SIGNAL 17
POTENTIAL.
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                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                 MEDLINE=88032846; PubMed=3667529;
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PIR; A29832; A29832.
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           HPI2_DEIRA
P13126;
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HPI2 DEIRA
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MEDLINE=94336695; PubMed=8058765;

MEDLINE=94336695; PubMed=8058765;

MEDLINE=94336695; PubMed=8058765;

Muchaer K., Berger R., Croce C.M., Canaani B.;

Huebner K., Berger R., Croce C.M., Canaani B.;

"Leucine-zipper dimerization motif encoded by the AF17 gene fused to recommend and acute leukemias.";

Proc. Natl. Acad. Sci. U.S.A. 91:8107-8111(1994).

"In SubCelliular LoCATION: Nuclear (Potential).

"In DISBASE: Involved in acute leukemias through a chromosomal ranslocation t(11,17)(q23;q21) that involves MLL/HRX and MLTG.

"The result is a rogue activator protein."

"The result is a rogue activator protein."

"In STMILARITY: Contains 2 PHD-type zinc fingers."

"In STMILARITY: HIGH, TO ARIO.

"In STMILARITY: HIGH, TO ARIO.

"In DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;

MWWH="http://www.infobiogen.fr/services/chromcancer/Genes/AF17.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO: CO.006355; P:regulation of transcription, DNA-dependent; TAS. InterPro; IPR001965; Znf_PHD.
Pfam; PF00628; PHD; 1.
PROSTIE; PG01359; ZF_PHD 1; 1.
PROSTIE; PG01359; ZF_PHD 1; 1.
PROSTIE; PG016; ZF_PHD_2; 2.
                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein; Zinc-finger; Repeat; Chromosomal translocation;
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Pred. No. 2.7e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F60042A6D3BF579E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEUKEMIA PATIENT)
                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-SER.
LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLY/SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHD-TYPE 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO-RICH.
GLN-RICH.
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GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1093 AA; 112021 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U07932; AAA21145.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:7138; MLLT6.
MIM; 600328; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      429 SPHVTGSGA 437
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                                                                                                              Homb sapiens (Human).
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proto-oncogene.
ZN FING 51
ZN FING 117
DOMAIN 190
                                                                                                                                                               NCBI_TaxID=9606;
                                                                               AF-17 protein.
MLLT6 OR AF17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; 138533;
AF17_HUMAN
P55198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE
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879 TPNVTGNSAL 888

AF17_HUMAN

RESULT 48

1 TPRVTGGGAM 10

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RC STRAINCEV. Columbia;

RX MEDLINE=20083488; PubMed=10617198;

RADINE=20083488; PubMed=10617198;

RADINE=20083488; PubMed=10617198;

RADINE=20083488; PubMed=10617198;

RADINE=20083488; PubMed=10617198;

RADINE=20083488; PubMed=10617188;

RADINE=20083488; PubMed=1061788;

RADINE=20083488; PubMed=10617818;

RADINE=20083488; PubMed=1061788;

RADINES B., Ansorge W., Brandt P., Garivell L.A., Rieger M., Medler B., Mache R., Mueller M., Reichert B., Portetelle D., Perez-Alonso M., Schnidtheini T., Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., RADINES B., Chuang Y.-J., Vandenbussche F., Radines Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F., Radines S., Hempel S., Rein Lankhorst R., Besteen M., Hauf J., Koetter P., RADIZER B., Reichert B., Peters S., van Staveren M., Dirkse W., Holzer B., Berneiser S., Hempel S., Feldpausch M., Lanmberth S., Van den Daele H., RADIZER B., Buysshaert C., Gielen J., Villarroel R., De Clercq R., Van Montagu M., Rogers J., Cronin A., Ouvill M.A., Bray-Allen S., And Moosy M., Rogers J., Cronin A., Ouvill M.A., Bray-Allen S., Radiner A., Balandream M.A., Lyne M., Benes V., Rechmann S., Argiriou A., Vitale D., Liguori R., Piravandi E., Astendar B., Schmidt W., Lecharry A., Casacuberta E., Gooke R., Berger C., Monfort A., Casacuberta E., Albons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., Rabbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., Rechmann D., Haase D., Lecharry A., Casacuberta E., Rabernann D., Heibnen D., Liguori S., Pradman D., Heibnen D., Jenner P., Heibnen D., Heibnen D., Lecharry S., Racorker S., Pradman D., Haase D., Lecharry S., Racorker S., Pradman D., Heibnen D., Schwarz S., Scholler P., Robers H., Weller B., Bent E., Johnson S., Tacon D., Jesse T., Rabizhen D., Lancke R., Meesen H.-W., Stocker S., Pradman D., Haase D., Lemker K., Meese B., Weller B., Bent E., Hebber R., Bent E., Bent E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PNK1 ARATH STANDARD; PRT; 870 AA.
Q8L5Y9; O49372; O49374;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Probable pantothenate kinase 1 (EC 2.7.1.33) (Pantothenic acid kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear ress).

Eukaryota, Viridiplantaa, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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0
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                                                                                                                                                                                                                                                    Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 138 BY SIMILARITY.
807 AA; 85231 MW; 66C274219155D091 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE
                           Pfam; PF00069; pkinase; I.
ProDom; PD00001; Prot_kinase; 1.
SMART; SM00564; PQQ; 4.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS001108; PROTEIN KINASE ST; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
InterPro, IPR008271; Ser_thr_pkin_AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AT4G32180 OR F10M6.180 OR F10N7.10.
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30
44
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                                                                                                                                                                                                                                                                                                       Phosphorylation.
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ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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STRAIN=CV. Columbia;

STRAIN=CV. Columbia;

MEDLINE=22954850; PubMed=14593172;

A Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

A Rarinada M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Torriumi M.J.,

A handa M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Torriumi M.J.,

A harawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

Hayashizaki Y., Johnson-Hopson C., Heuan V.W., Iida K., Karnes M.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Sakurai T.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Sakurai T.,

Sattou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L., Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threaded J., Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J., Latreille P., Coutney L., Cloud J., Abbott A., Scott K., Johnson D., A minx P., Bentley D., Fulton B., Miller N., Greco T., Kremp K., Armer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W., Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Anna B., Marra M.A., Martlenssen R., McCombie W.R., Cohn S., Kara M.A., Martlenssen R., McCombie W.R., Chen B., Marra M.A., Martlenssen R., McCombie W.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphopantothenate.
-!- ENZYME REGULATION: Regulated by feedback inhibition by malonyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 302:842-846(2003).
-!- FUNCTION: Plays a role in the physiological regulation of the intracellular CoA concentration (By similarity).
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Pred. No. 2.2e+02;
1: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGREAMS; TIGRO0555; panK eukar; 1.
Transferamse; Kinase; ATP-Dinding; Coenzyme A biosynthesis.
SEQUENCE 870 AA; 96234 MW; 23CECA42A3D8EA6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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EMBL, ALICESO, CAB59395.1, ALT_SEQ.
EMBL, ALO21636; CAA16571.1; ALT_SEQ.
EMBL, AX099839; AAM20690.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002791; DUF89.
InterPro; IPR004567; PanK eukar.
Pfam; PP01937; DUF89; 1.
Pfam; PF03630; Fumble; 1.
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85.7%;
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Best Local Similarity
6, Conservative
                                                                                                                                                                                                                                                                                                                                                 Nature 402:769-777(1999).
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SMART:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                    Matsumoto A., Hong S.K., Ishizuka H., Horinouchi S., Beppu T., "Phosphorylation of the AfsR protein involved in secondary metabolism in Streptomyces species by a eukaryotic-type protein kinase."; Gene 146:47-56(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ueda K., Umeyama T., Beppu T., Horinouchi S.;
"The aerial mycellum-defective phenotype of Streptomyces griseus resulting from A-factor deficiency is suppressed by a Ser/Thr kinase of S. coelicolor A3(2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLOBAL REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taylor K.,
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.E., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Tarper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete genome sequence of the model actinomycete Streptomyces
                                                   .
0
                                                                                                                                                                                                                                                        Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinomycetales;
                         62.3%; Score 33; DB 1; Length 692; 75.0%; Pred. No. 1.7e+02; i.ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matsumoto A., Hong S., Ishizuka H., Horinouchi S., Beppu Umeyama T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 692 AA; 76745 MW; 0E58310C4F3EFD80 CRC64;
                                                                                                                                                                  AFSK STRCO STANDARD; PRT; 799 AA. P54741; Q9F365; Q91002; 001-007-1996 (Rel. 34, Created) 16-007-2001 (Rel. 40, Last sequence update) 16-007-2003 (Rel. 42, Last annotation update) Serine/threconine protein kinase afsk (EC 2.7.1.37). AFSK OR SCO4423 OR SCFF11.21 OR SCD6.01.
                                                                                                                                                                                                                                                                               Streptomycineae; Streptomycetaceae; Streptomyces.
                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                   STRAIN=A3(2);
MEDLINE=94341568; PubMed=8063104;
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96186909; PubMed=8635757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coelicolor A3(2).";
Nature 417:141-147(2002)
                                                    Conservative
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                                                                                                      513 TPNETGGG 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 169:91-95(1996)
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                                   Local Similarity
les 6; Conserva
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                               1 TPRVTGGG
                                                                                                                                                                                                                                                                                              NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=A3 (2);
      SEQUENCE
                             Query Match
                                                                                                                                                       AFSK_STRCO
                                                        Matches
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and for commercial
                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE=90186909; PubMed=8635757; Ueda K., Umeyama T., Beppu T., Horinouchi S.; Umeyama T., Beppu T., Horinouchi S.; Umeyama T. Beppu T., Horinouchi S.; Ireptomyces griseus resulting from A-factor deficiency is suppressed by a Ser/Thr kinase of S. coelicolor A3(2)."; Gene 169:91-95(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FINCTION: INVOLVED IN THE REGULATION OF SECONDARY METABOLLSM:
PHOSPHORYLATING, ON BOTH SER AND THR, THE AFSR GLOBAL REGULATY
PROTEIN INVOLVED IN THE CONTROL OF SECONDARY METABOLLSM (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces griseus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
W, 4BE9BED4169F6F5B CRC64;
     Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serine/threonine protein kinase afsK (EC 2.7.1.37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 1;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                807 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
        and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                entities requires a license agreement (Se
or send an email to license@lsb-sib.ch).
                                                                                                                                                                         PhosSite, P54741; -.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser thr pkin AS.
Pfan; PF00069; pkinase; I.
ProDom; PD000001; Prot_kinase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphorylation; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PhosSite; P54742; -.
InterPro; IPR000719; Prot kinase.
                                                                                                                                                  AL939120; CAD55483.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 138 B
799 AA; 83787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.3%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D45246; BAA08203.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                     EMBL; D45382; BAA08229.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               648 PAVTGGG 654
                                                                                                                                                                                                                                                                                                                   SM00564; PQQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PRVTGGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY)
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        modified a
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                         AVYGHHWRASTGDARSDCAPSPRIAPPGAPLALTAHPGAGS
                                                                                                                                                                                                                                                    ADTPETQDSVSSSRKPASA -> SLRPPLASLDRRRAFRLR
PQPSHRSPRGPSSPHCTPGCGLGRHAGDAGFGLQQSKASLR
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ishigami A., Guerrin-Weber M., Sebbag M., Serre G., Senshu T.;
"Molecular cloning of peptidylarginine deiminase type I cDNA from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      citrulline + NH(3).
-!- COFACTOR: Requires calcium ions (By similarity).
-!- SIMILARITY: Belongs to the protein arginine deiminase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
LoCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last smootation update)
Protein-arginine deiminase type I (EC 3.5.3.15) (Peptidylarginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                            7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
S-palmitoyl cysteine (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the deimination of arginine residues of proteins (By similarity).
-!- CATALYTIC ACTIVITY: Protein L-arginine + H(2)0 = protein L-
                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                     62.3%; Score 33; DB 1; Length 561; 66.7%; Pred. No. 1.4e+02; ive 1; Mismatches 2; Indels
                                                                                                   CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                             B6537DCAD4F7BE27 CRC64;
                                                                4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                    CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        663 AA.
                                                                                            5 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                 GLY-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004303; Prot_arg_deim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB033768; BAA85771.1; -.
                                                                                                                                                                                                                                                                                              561 AA; 59354 MW;
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGNC:18367; PADI1
                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
            2 PRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                        43 PGATGGGAV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Epidermis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human epidermis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                          60
76
413
21
416
424
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PADII OR PDII.
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                                                                                                        DOMAIN
TRANSMEM
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TRANSMEM
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CONFLICT
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J., Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z., Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.; "Genome-based analysis of virulence genes in a non-biofilm-forming Staphylococcus epidermidis strain (ATC 12228)."; Mol. Microbiol. 49:1577-1593(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
EF-G/EF-2 subfamily.
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the nascent protein chain from the A-site to the P-site of the
                                                                                                                          0
                                                                                         Length 663;
                                                                                                                      1; Indels
Pfam; PF03068; PAD; 1.
Hydrolaes; Calcium-binding; Multigene family.
CA BIND 506 517 BF-HAND (POTENTIAL).
CA BIND 77 74607 MW; 0BDBD460634EEZD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TICRFAMS; TICR00231; small GTP; 1.
PROSITE; PS00301; EFACTOR GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
                                                                                         62.3%; Score 33; DB 1; I
75.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                   10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY.
                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HANAP, MF 00054; -; 1.
InterPro; IRR000795; BF GTPbind.
InterPro; IPR0009025; BFG III V.
InterPro; IPR000517; BFG IV.
InterPro; IPR005517; BFG IV.
InterPro; IPR00525; Small GTP.
InterPro; IPR005000; Tanslat_factor.
Pfam; PF00679; BFG C; 1.
Pfam; PF03764; BFG C; 1.
Pfam; PF03764; BFG C; 1.
Pfam; PF03144; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE016745; AA003908.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00315; ELONGAINFCT
                                                                                                                                                                                                                                                                                                                                     10-OCT-2003 (Rel. 42, Last a Elongation factor G (EF-G).
                                                                                         Query Match
Best Local Similarity 75.03
Matches 6; Conservative
                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
23
84
137
                                                                                                                                                                                        415 SPPVTGGG 422
                                                                                                                                                        1 TPRVTGGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=ATCC 12228;
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                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=12950922;
                                                                                                                                                                                                                                                                                                                                                                       FUSA OR SE0311
                                                                                                                                                                                                                                                                        EFG STAEP
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NP_BIND
NP_BIND
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EFG_STAEP
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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Bouck J., Broketen P., Brother P., Charley S., Bouck J., Broketen P., Brother P., Charley S., Burler S.M., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Burtis K.C., Cawley S., Dahlke C., Davemport L.B., Davies P., Charler B., Davies P., Dandy D.B., Dong Z., Mays A.D., Dew I., Dietz S.M., Dodgon K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rosler C., Gabrielian A.E., Garg N.S., Genger, K., Ferraz C., Ferraz C., Ferriera S., Fleischmann W., Rosler C., Gabrielian A.E., Garg N.S., Galbart W.M., Glasser K., RA, Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Hostin R.J., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Hostin B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA, Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Rathei B.R., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., A., Merkei B., McIntosh T.C., Morris J., McBherson D.L., RA, Merkei B., McIntosh T.C., Morris J., McBon D.L., RA, Melson D.L., Markei B., McIntosh T.C., Morris J., Moshrefi A., Rohason D.K., Nelson K., Siden H., Wang X., Ra, Rainson K.A., Mison K., Nixon K., Murphy D., Puri V., Rese M.G., RA, Rainson K.A., Nixon K., Nusskern D.R., Porl Smith T., Spher E., Siden H., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Williams S.M., Woodage T., Weinstock G.M., Weissenbach J., RA, Reiner K., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O., Ra, Zheng X. H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O., The Strong R. The Genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U61852; AAC47551.1; -. FlyBase; FBgn0011818; oaf.
GO; GO:0016321; P:female meiosis chromosome segregation; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Merli C., Bergstrom D.E., Cygan J.A., Blackman R.K., "Promoter specificity mediates the independent regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AT FIRST PROTEIN.
AT FIRST SHORT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-89 FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> G (IN REF. 1).
-> H (IN REF. 1).
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POLY-THR.
POLY-LEU.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003583; AAF51246.1; ALT TERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96217926; PubMed=8675012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L31349; AAC37219.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Developmental protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neighboring genes.";
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472
472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINES=5514877; PubMed=7815325; O., Mosley M.J., Wilson K.H., Schwinn D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H., Worman N.P., Campbell S., Fidock M.D., Furness L.M., Parry-Smith D.J., Peter B., Bailey D.S., "Cloning and pharmacological characterization of human alpha-1 adrenergic receptors: sequence corrections and direct comparison with
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other species homologues.";
J. Pharmacol. Exp. Ther. 272:134-142 (1995).

-!- FUNCTION: This alpha-adrenagic receptor mediates its effect through the influx of extracellular calcium.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Vas deferens, hippocampus, cerebral cortex, aorta, brain stem, heart and spleen.
-!- SUMLIARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lomasney J.W., Cotecchia S., Lorenz W., Leung W.-Y., Schwinn D.A., Yang-Feng T.L., Brownstein M., Lefkowitz R.J., Caron M.G., "Molecular cloning and expression of the cDNA for the alpha 1A-adrenergic receptor. The gene for which is located on human
                                                                                                                                                                                                                                                                                                                   01-MAR-1992 (Rel. 21, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Alpha-1D advencyic receptor (Alpha 1D-adrenoceptor) (Alpha-1A ADRAID OR ADRAIA)
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PROSITE; PS50262; G PROTEIN RECEP F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Multigene family; Phosphorylation; Lipoprotein; Palmitate.
DOMAIN
                                                       62.3%; Score 33; DB 1; Length 487; 66.7%; Pred. No. 1.2e+02; ive 1; Mismatches 2; Indels
413 413 A -> T (IN REF. 1).
487 AA; 53728 MW; FOD7A117BE358B3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Sprague-Dawley, TISSUE-Brain cortex;
MEDLINE-91177889; PubMed=1706716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Biol. Chem. 266:6365-6369(1991).
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PRINTS; PR00237; GPCRRHODOPSN.
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EMBL; L31771; AAB59704.1; -.
PIR; A38731; A38731.
                                                                                  Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                    373 TATITGGGA 381
                                                                                                                                                1 TPRVTGGGA 9
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        CONFLICT
                                                                                                                                                                                                                                                                                          ALAD RAT
                                                                 Query Match
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1 (POTENTIAL).

*TRANSMEM* 

CONFLICT

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SOTT TTT TTT SOLUTION SOLUTION
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MEDLINE-2238825; PubMed=12477932,

RIJUNE-2238825; PubMed=12478,

RIJUNE-2238825; PubMed=12478,

RIJUNE-2238825; PubMed=12478,

RIJUNE-2238825; PubMed=12488,

RIJUNE-238828,

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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
-!- FUNCTION: INVOLVED IN CELL CYCLE ARREST WHEN DNA DAMAGE HAS
OCCURRED OR WHEN UNLIGHED BAD CDC25C. PHOSPHORYLATION OF
PHOSPHORYLATES CDC25A, CDC25B AND CDC25C. PHOSPHORYLATION OF
CDC25C. CREATES A BINDING SITE FOR 14-3-3 BROTELIN WHICH INNIBITS
CDC25C. THIS PREVENTS ACTIVATION OF THE CDC2-CYCLIN B COMPLEX AND
PREVENTS MITOTIC ENTRY. PHOSPHORYLATES CDC25C ON SERINB-216.
-:- SUBCELLULAR LOCATION: Nuclear.
-:- TISSUE SPECIFICITY: Expressed ubiquitously with the most abundant
expression in thymus, testis, small intestine and colon.
                                                                                                                                                                                                Semba S., Ouyang H., Han S.-Y., Kato Y., Horii A., "Analysis of the candidate target genes for mutation in microsatellite instability-positive cancers of the colorectum, stomach, and endometrium.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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BAA84577.1; JOINED.
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                                                                                                                                                                               MEDLINE=20184068; PubMed=10717241;
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Curr. Biol. 7:977-986(1997)
                                                                                                                    SEQUENCE FROM N.A.
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BAA84577.1; BAA84577.1;

BAA84577.1; BAA84577.1;

AB032384; AB032383;

EMBL;

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AB032385; 1 AB032386; 1

EMBL; EMBL;

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DR GK; Uttalong: 1.

BR MIN; 603078; -.

DR GO; GO:0006711; C:meiotic chromosome; TAS.

GO; GO:000077; F:protein kinase activity; TAS.

BR GO; GO:000077; F:protein kinase activity; TAS.

BR GO; GO:00007276; F:protein kinase response, signal transduction re. .; TAS.

BR GO; GO:00007131; F:mediotic recombination; TAS.

BR GO; GO:00007131; F:mediotic recombination; TAS.

BR GO; GO:000079; P:regulation of Cell proliferation; TAS.

BR GO; GO:000079; P:regulation of Cell proliferation; TAS.

BR InterPro; IPR00229; Prot kinase.

BR InterPro; IPR002290; Ser thr pkinase.

BR PFO0000; PRO0001; Prot kinase; 1.

BR PROSTIE; PRO00001; Prot kinase; 1.

BR PROSTIE; PRO01001; PROTEIN KINASE ATP; 1.

BR PROSTIE; PROSTIEN KINASE DOM; 1.

RW Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle; RW DNA damage; Nuclear protein; Phosphorylation; 3D-structure.

FT ACT-SITE 130 BY SIMILARITY).

FT ACT-SITE 130 BY SIMILARITY.

FT ACT-SITE 130 BY SIMILARITY.
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MEDLINER_20196006; PubMed=10731132;
Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Berkeley; TISSUB=Embryo;
MEDINE=5928666; PubMed=7768442;
Bergetrom D.E., Merli C.A., Cygan J.A., Shelby R., Blackman R.K.;
"Regulatory autonomy and molecular characterization of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota, Neoptera, Endopteray, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxIb=7227;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Out at first protein (Contains: Out at first short protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 1; Length 476; Pred. No. 1.2e+02; 0; Mismatches 1; Indels
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EMBL; AF527555; AAM78553.1; -. EMBL; BC004202; AAH04202.1; -. EMBL; BC017575; AAH17575.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                out at first gene.";
Genetics 139:1331-1346(1995).
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 85...
6; Conservative
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                                                                    PDB; 11A8; 18-APR-01.
Genew; HGNC:1925; CHEK1.
GK; 014757; -.
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MEDLINE=87146423; PubMed=3029698;
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CHK1_HUMAN
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N-LINKED (GLCNAC. .) (POTENTIAL).
MIQDPDSDQPLNSLDVKPLRKPRIPMETFRK -> MSNPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Shufflon protein B'.
Bscherichia coli.
Plasmid Incl1 R64, and Plasmid Incl1 Collb-P9.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
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0
         R MIM, 606565; -. Gintegral to membrane; NAS. GO; GO:0016021; C:integral to membrane; NAS. R GO; GO:0006508; P:serine-type endopeptidase activity; NAS. GO; GO:0006508; P:serine-type endopeptidase activity; NAS. R InterPro; IPR001903; Cys Ser trypsin.

R InterPro; IPR00172; LDL Feceptor_A.

R InterPro; IPR001134; Peptidase S1A.

R InterPro; IPR001190; Stor receptor.

R Pfam; PF00089; trypsin; 1.

R PRONTS; RR00190; Stor receptor.

R MART; SM0020; LDLA; 1.

R SMART; SM0020; Tryp SPC; 1.

R RAMAT; SM0020; Tryp SPC; 1.

R ROSITE; PS00420; SRCR 1; FALSE NEG.

R ROSITE; PS00420; SRCR 1; FALSE NEG.

R ROSITE; PS00135; TRYPSIN DOM; 1.

R RROSITE; PS00135; TRYPSIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.3%; Score 33; DB 1; Length 437; 85.7%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Serine protease; Transmembrane; Signal-anchor. CytyopiasMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLUIAR (POTENTIAL)
LDL-RECEPTOR CLASS A.
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 444 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae; Escherichia.
NCBL TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 AA; 48204 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 TPRVVGG 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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P09748;
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                                                                                                                                                                                                                                                                                                                    "Cloning and nucleotide sequence of the Collb shufflon.";
plasmid 22:180-184[1989].
-!- MISCELLANEOUS: THIS PROTEIN IS EXPRESSED BY A SHUFFLON (=
CLUSTERED INVERSION REGION THAT WORKS AS A BIOLOGICAL SWITCH). THE
ORFS OF THIS REGION SHARE A CONSTANT N-TERMINUS, WHILE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98044285; PubMed=9382850;
Flaggs G., Plug A.W., Dunks K.M., Mundt K.E., Ford J.C.,
Quiggle M.R.E., Taylor E.M., Westphal C.H., Ashley T., Hoekstra M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sanchez Y., Wong C., Thoma R.S., Richman R., Wu Z., Piwnica-Worms H., Elledge S.J.;
Komano T., Kubo A., Nisioka T.; "Shufflon: multi-inversion of four contiguous DNA segments of plasmid R64 creates seven different open reading frames."; Nucleic Acids Res. 15:1165-1172(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Conservation of the Chkl checkpoint pathway in mammals: linkage of DNA, damage to Cdk regulation through Cdc25."; Science 277:1497-1501(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.3%; Score 33; DB 1; Length 444
75.0%; Pred. No. 1.1e+02;
rative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 444 VARIABLE REGION.
444 AA; 46945 MW; ESES17667FE46304 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
serine/threonine-protein kinase Chkl (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONSTANT REGION.
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                                                                                                                                                                                        SEQUENCE OF 362-444 FROM N.A. PLASMID=Incil Colib-P9; MEDLINE=90160874; PubMed=2623084; Kim S.R., Komano T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB027308; BAA77987.1; -.
EMBL; D90039; BAA14091.1; -.
PIR, D26421; D26421.
INCETEC; IPR007001; Shufflon N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
FUNCTION: Probable protease. Seems to be capable of activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL)
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0
                           -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
-!- SIMILARITY: Belongs to peptidase family $1.
-!- SIMILARITY: Contains 1 LDL-receptor class A domain.
-!- SIMILARITY: Contains 1 SRCR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.3%; Score 33; DB 1; Length 435; 85.7%; Pred. No. 1.1e+02; 1.ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase, Serine protease, Transmembrane, Signal-anchor.
DOMAIN 1 30 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
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BY SIMILARITY
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                                                                                                                                                                                                                                                                                          musi, musi.zosad., imperation.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR002172; LDL_receptor_A.
InterPro; IPR00124; Peptidase_S1.
InterPro; IPR001124; Peptidase_S1.
InterPro; IPR001190; Srcr_receptor_Pfam; PP00085; Irypsin; 1.
Pfam; PP00089; trypsin; 1.
PRNIWS; PR001229; LDLRA_1; PALSE_NEG.
PROSITE; PS01209; LDLRA_1; PALSE_NEG.
PROSITE; PS01209; LDLRA_2; PALSE_NEG.
PROSITE; PS00420; SRCR_1; PALSE_NEG.
PROSITE; PS00420; SRCR_1; PALSE_NEG.
PROSITE; PS001315; TRYPSIN_HIS; 1.
PROSITE; PS001315; TRYPSIN_HIS; 1.
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Q9NRS4; Q9NZA5;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                       EMBL; AY043240; AAK85307.1; --
EMBL; BC021368; AAH21368.1; --
HSSP; P00761; IAN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                    MGD; MGI:2384877; Tmprss4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 385
203
81
90
181
191
308
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Best Local Similarity
                                                                                                                                                                                                                                                                  MEROPS; S01.034;
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ACT SITE
ACT SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RC TISSUE-PROTECTES:

RA MEDLINE-22388257; PubMed=12477932;

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.E., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bratchenco L., Marusina K., Farmer A.A., Waln G.M., Hong L., Schaefer C.F., Stapleton M.J., Uddin T.B., Poefers G.J., Abramson R.D., Mullaby S.J.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Garninci P., Prange C.,

RA Bosak S.A., McEwan P.W., Poefers G.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McEwan P.W., Sodergren B.J., Lu X., Gibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,

RA Fahey J., Helton E., Ketteman M., Maden A., Rodrigues S., Sanchez A.

RA Batesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RAC (By similarity): Type II membrane protein (Potential):

C. --- FUNCTION: Probable protease. Seems to be capable of activating

RAC (By similarity): Type II membrane protein (Potential):

and ampullary cancer. Very weak expression in normal

and ampullary: Contains I Indi-receptor class A domain.

C. --- SIMILARITY: Contains I SRCR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastric, colorectal
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Transmembrane protease, serine 4 (EC 3.4.21.-) (Membrane-type serine
                                                                                                                                                                                                                                                                                                                                                                                                                                  Smeekens S.S., Lorimer D.D., Wang E., Hou J., Linnevers C.; MT-SP2, a novel type II membrane serine protease expressed in trachea, colon, and small intestine: identification, cloning, and chromosomal localization.";
                                                                                                                                                                                                                                                                         Wallrapp C., Haehnel S., Mueller-Pillasch F., Burghardt B., Iwdmura T., Ruthenbuerger M., Lerch M.M., Adler G., Gress T.M.; An novel transmembrane serine protease (TMPRSS3) overexpressed in pancreatic cancer.";
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-Pancreatic carcinoma;
MEDLINE-20283276; PubMed=10825129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF179224; AAF74526.1; --
EMBL; AF216312; AAF31436.1; --
EMBL; BC011703; AAH11703.1; --
HSSP; P00763; 1DPO.
MEROPS; S01.034; --
Genew; HGNC:11878; TMPRSS4.
                                                                                                                                                                                                                                                                                                                                                                             Cancer Res. 60:2602-2606(2000).
                                                                           (MT-SP2).
                                                                                                                    Homo sapiens (Human)
                                                                      protease 2) (MT-SP2
TMPRSS4 OR TMPRSS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Pancreas;
                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEY SEQUENCE FROM N.A.

RAY TISSTER=COLON. Bye, Muscle, Pancreas, and Skin;

RAY TISSTER=COLON.

RAY STANDENCE R.D., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

RAY Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RAY Altechul S.F., Jeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RAY Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RAY Diacrhenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RAY Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RAY Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

RAY Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RAY Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RAY Michards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

RAY Paleson M., Sodergren E.J., Lu X., Gibbs R.A.,

RAY Martay J., Helton E., Ketteman M., Machenko Y., Bouffard G.G.,

RAY Matting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RAY Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RAY Schnerch A., Schain J.E., Jones S.J.M., Marra M.A.;

Redriguez A.C., Grimwood J., Schwarra M.A.;

Redriguez A.C., Grimwood J., 
                                                    Bagni C., Mariottini P., Annesi F., Amaldi F.,
"Human ribosomal protein L4: cloning and sequencing of the cDNA and
primary structure of the protein.";
Biochim. Biophys. Acta 1216:475-478(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21864036; PubMed=11875025; Kawasaki K., Kato S., Higa S., Yobhihama M., Uechi T., Asakawa S., Kawasaki K., Kenmochi N.; Maeda N., Minoshima S., Tanaka T., Shimizu N., Kenmochi N.; "The human ribosomal protein genes: sequencing and comparative
                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                              Bagni C.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, X73974; CAA52154.1; -.
EMBL, L20868; AAA60281.1; ALT_SEQ.
EMBL, D23660; BAA04887.1; -.
                                         MEDLINE=94092742; PubMed=8268230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, BC007996; AAH07996 1).
EMBL, BC01051, AAH10888 1;
EMBL, BC010151, AAH10151.1;
EMBL, BC014653; AAH14653.1;
EMBL, AB061820; BAB79458 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, BC001365; AAH01365.1;
EMBL, BC005817; AAH05817.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC007748; AAH07748.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-2DPAGE; P36578; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analysis of 73 genes.";
Genome Res. 12:379-390(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:10353; RPL4.
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               rissuE≈Lymphoma;
                                                                                                                                                                                                    REVISIONS.
                                                                                                                                                                                                                                                                                                                                                       Kato S.;
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RADELINES-238825; PubMed=12477932;
RADELINES-238825; PubMed=12477932;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Alusner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Alusner R.D., Colling F.S., Wagner L., Shemmen C.M., Bhat N.K.,
Aluschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Aluschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Biachenko L., Marusina K., Former A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.M., Ogacria A.M., Gay L.J., Hulyk S.W.,
RA Ribards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Modriguez A.C., Grimwood J., Schwutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schwutz J., Marra M.A.,
RA Rodriguez A.C., Grimwood J., Schwutz J., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length
RT Fucc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                       ·.
                      GO:0005842; C:Cytosolic large ribosomal subunit (sensu Eu. . .; TAS. GO:0003723; F:RNA binding; TAS. GO:0003735; F:Rtructural constituent of ribosome; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22144321; PubMed=12149280;
Wagniaux G., Vallet V., Jaeger N.F., Hummler E., Rossier B.C.;
Vagniaux G., Vallet V., Jaeger N.F., Hummler E., Rossier B.C.;
"Synergistic activation of ENaC by three membrane-bound channel-activating serine proteases (MCAPI, mCAP2, and mCAP3) and serum- and aplucocorticoid regulated Kinase (SgK1) in Xenopus oocytes.";

J. Gen. Physiol. 120:191-201(2002).
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Transmembrane protease, serine 4 (EC 3.4.21.-) (Channel-activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamhalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                 Length 427;
                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                      3 3 C -> V (IN REF. 1).

36 36 I -> M (IN REF. 1).

63 63 S -> R (IN REF. 1).

147 147 V -> F (IN REF. 1).

201 201 MISSING (IN REF. 1).

427 AA, 47697 MW, 4785ED31699CD792 CRC64;
                                                                                                                                                                                                                                                                                                                                                    62.3%; Score 33; DB 1; I
85.7%; Pred. No. 1.1e+02;
                                                                                       CO, GO:0006412; P:protein biosynthesis; TAS. InterPro; IPR002135; Ribosomal L4/LiE. Pfam. PF00573; Ribosomal L4: 1. Pfam. PF00573; Ribosomal L4: 1. PROSTIE; PS00939; RIBOSOMAL_LIE; 1.
                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                         LYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-OCT-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                             85.78;
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (mCAP2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 PRVRGGG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 6; Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PRVTGGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=10090;
                                                                                                                                                                               Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPRSS4 OR CAP2
                180479; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protease 2)
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                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          Query Match
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NON TER 1 1 SEQUENCE 420 AA; 47384 MW; D971FC2950A387BB CRC64;
                                                                                                                                                                                                                                                                    50S ribosomal protein L4 (L1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X82180; CAA57671.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                STANDARD;
                                                      Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 PRVRGGG 83
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                                                                                                                           76 PRVRGGG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribosomal protein.
                                                                                                2 PRVTGGG 8
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPL4 OR RPL1.
                                                                                                                                                                                                                                                                                      RPL4 OR RPL1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                     Query'Match
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                                                                                                                                                                          RESULT 34
                                                                     Matches
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                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Weneration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canis familiaris (Dog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the L4E family of ribosomal proteins.
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o
                                                                                                                                                                                                                                                                                                                                                                                                          161 161 Y -> F (IN REF. 1; BAB27375).
419 AA; 47153 MW; E736E656A60BE85B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.3%; Score 33; DB 1; Length 419; 85.7%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
60S ribosomal protein L4 (L1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF00573; Ribosomal L4; 1.
PROSITE; PS00939; RIBOSOMAL LIE; FALSE NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nterPro; IPR002136; Ribosomal_L4/L1E.
                                                                                                                                                                                                                                                                                                                                        InterPro, IPR002136, Ribosomal L4/L1E.
                                                                                                                                                                                                                                                                                                                                                                                                   LYS-RICH
                                                                                                                                                                                                                                                                                                                                                                     PROSITE, PS00939; RIBOSOMAL LIE; 1. Ribosomal protein.
                                                                                                                                                                                                                                                                                EMBL; AK008098; BAB25458.1; -.
EMBL; AK011068; BAB27375.1; -.
EMBL; BC003459; AAH03459.1; -.
MGD; MGI:1915141; 2010004723Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X99909; CAA68182.1; -.
                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00573; Ribosomal_L4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 PRVRGGG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PRVTGGG 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Mongrel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sandholzer U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPL4 OR RPL1
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Q28346;
                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                      Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAINE-Sprague-Dawley, TISSUE-Liver,
MEDLINE-Sprague-Dawley, TISSUE-Liver,
MEDLINE-S6024571; PubMed=7575549;
Chan Y.-L., Olvera J., Wool I.G.;
"The primary structures of rat ribosomal proteins L4 and L41.";
Biochem. Biophys. Res. Commun. 214:810-818(1995).
-: SIMILARITY: Belongs to the L4E family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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0
62.3%; Score 33; DB 1; Length 420;
85.7%; Pred. No. 1e+02;
ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.3%; Score 33; DB 1;
Best Local Similarity 85.7%; Pred. No. le+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236578; P39029; Q96929; 01-UNN-1994 (Rel. 29, Created) 28-FBS-2003 (Rel. 41, Last sequence update) 605 ribosomal protein L4 (L1).
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Pfam; PF00573; Ribosomal L4; 1.
PROSITE; PS00939; RIBOSOMAL L1E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYS-RICH
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PRINTS; PR00723; SUBTILISIN.
                                                                SIGNAL
                                                                          PROPEP
                                                                                      CHAIN
                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96004470; PubMed=7551039; Reeves R.A., Bergquist P.L.; Mudic G.K., McHale R.H., Saul D.J., Reeves R.A., Bergquist P.L.; Mudic electroning a thermophilic alkaline serine proteinase from "A gene encoding a thermophilic alkaline serine proteinase from Thermus sp. strain Rt41A and its expression in Escherichia coli."; Microbiology 141:1731-1738(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PTM: Contains 4 Cys residues that form two disulfide bonds.
-!- PTM: This proteinase has a 0.7% carbohydrate content.
-!- SIMILARITY: Belongs to peptidase family 58.
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0
                                                                                                                                                                                                     62.3%; Score 33; DB 1; Length 408; 85.7%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                              FOULTY, 01-1992 (Rel. 24, Created) 01-DECT-1995 (Rel. 34, Last sequence update) 01-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) Extracellular serine proteinase precursor (EC 3.4.21.-).
                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                             408 AA; 44869 MW; DAD8C75E8CDA7594 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 131-145, AND CHARACTERIZATION.
                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000209; Peptidase 58.
InterPro; IPR000437; Prok_lipoprot_S.
Pfam; PF00082; Peptidase_S8; 1.
                                                                                                                                 InterPro; IPR002136; Ribosomal L4/L1E.
Pfam; PF00573; Ribosomal L4; 1-
PROSITE; PS00939; RIBOSOMAL L1E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U17342; AAA82980.1; -.
HSSP; O99405; 1MPT.
                                                                                                                        EMBL; AF134732; AAD32206.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                (Btrain Rt41A).
                                                                                                                                                                                                  Query Match
Best Local Similarity 85...
Best G; Conservative
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; S08.008; -
                                                                                                                                                                                                                                                                                 84 PRVPGGG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         2 PRVTGGG 8
                                                                                                                                                                     Ribosomal protein.
SEQUENCE 408 AA;
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                                                                                                                                                                                                                                                                                                                                              THESE
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RC STRAIN=CS7BL/6J; TISSUB=Embryonic liver, and Small intestine;

RC MEDLINE=2108560; PubMed=11217851;

RA MEDLINE=2108560; PubMed=11217851;

RA ARAWAW T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Gasavant T.,

RA Adoca K., Matsuda H.A., Ashburner M., Batalov S., Gasavant T.,

RA RAGORA K., Matsuda H.A., Sukuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Sukuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furumo M., Anno H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J. Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Macamiya M., Sako K., Schoenbach C., Seya T., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA HAVASHISANI V.,
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MEDLINE-2238825).

Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Popkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Staplenon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Reha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                 CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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                                                                                                                                                                                            EXTRACELLULAR SERINE PROTEINASE.
                                                                                                                                                                                                                                                                                                                                                                                            62.3%; Score 33; DB 1; Length 408; 60.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                             7F48716F541A6CA7 CRC64;
PROSITE; PSO0136; SUBTILASE ASP; 1.
PROSITE; PSO0137; SUBTILASE HIS; 1.
PROSITE; PSO0138; SUBTILASE SER; 1.
Hydrolase; Serine protease; Glycoprotein; Signal.
1 19
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28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 42, Last sequence update)
60S ribosomal protein L4 (L1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                              42284 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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Best Local Similarity
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131
169
169
202
354
354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RL4 MOUSE
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ACT_SITE
SEQUENCE
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Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

SECUENCE FROM N.A.

Drosophila melanogaster (Fruit fly).

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Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C., Magner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N., Parnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J., Richoff K., Toth K., King L., Bahret A., Miller B., Marra M.A., Martienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroff I., Britan K.-D., Terryn N., Hartley N., Bent B., Johnson S., Britan K.-D., Terryn N., Hartley N., Bent B., Johnson S., A., McCullagh B., Robben J., Grymonprez B., Zimmermann W., Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W., Wedler U., Wedler H., Balke K., Wedler E., Peters S., Weitzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S., Weitzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S., Weitzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S., A Bents O., Lemcke K., Kolesov G., Mayer K.F.X., Rudd S., Schoof H., Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. Columbia;
Desprez T., Amselem J., Chiapello H., Rouze P., Caboche M., Hofte H.;
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. Columbia;
Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.,
Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the LAE family of ribosomal proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Columbia;
Berthomieu P., Guerrier D., Giraudat J.;
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
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E -> D (IN REF. 4).
, 026FC2852B7A2038 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00939; RIBOSOMAL_LIE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL162973; CAB86041.1; -. EMBL; Z18118; CAA79104.1; -. EMBL; Z18460; CAA79191.1; -. EMBL; Z17589; CAA791904.1; -. PIR; T48308; T48308.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thaliana
                                             SOLUTION NEW YORKS STATE STATE
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01-MAR-1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 10, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) 60S ribosomal protein L4 (L1).

SEPPRE

RPL4 OR RPL1.

407 AA.

STANDARD;

RL4 DROME P09180;

RL4_DROME RESULT 29

83 PRVPGGG 89

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Bergeron; TISSUB=Mesocarp;
Mbeguie-A-Mbeguie D., Fils-Lycaon B.R.;
"Molecular cloning and nucleotide sequence of a 608 ribosomal protein
11 from apricot (Prunus armeniaca cv. Bergeron).";
Submitted (WAR-1999) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: Belongs to the L4E family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prunus armeniaca (Apricot).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Core endicots; rosids; Spermatophyta; Magnoliophyta; endicotyledons; core endicots; rosids; Spermatophyta; Roseles; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                          STRAIN=Oregon-R;
MEDLINE=89098414; PubMed=2492096;
MEDLINE=89098414; PubMed=2492096;
Rafti F ., Gargiulo G., Manzi A., Malva C., Graziani F.;
Rafti F ., Gargiulo G., Manzi A., Malva C., Graziani F.;
"Sequence of the ribosomal protein con CDNA of D. melanogaster homologous
to the L1 ribosomal protein gene of X. laevis.";
Nucleic Acids Res. 17:456-456(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                               "Isolation and structural analysis of a ribosomal protein gene in
                                                                                                                                                                                                                                                     MEDLINE-89262486; PubMed-3133637;
Rafti F., Gargiulo G., Manzi A., Malva C., Grossi G., Andone S.,
Graziani F.;
                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the L4E family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.3%; Score 33; DB 1; Length 407; 85.7%; Pred. No. 1e+02; 1; Indels :ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 117 K -> R (IN REF. 2).
407 AA; 45755 MW; F35D7898770B043C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Last Sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 60S ribosomal protein L4 (L1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002136; Ribosomal L4/L1E. Pfam; PF00573; Ribosomal L4; 1. PROSITE; PS00939; RIBOSOMAL L1E; 1.
                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 16:4915-4926(1988).
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                                                                                                                                                                                                                                                 SECUENCE OF 63-186 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=36596;
                                                                                                                                                                                                                                                                                                                                             D.melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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MEDLINE=21016720; PubMed=11130713;
Salanoubat M., LemcKe K., Rieger M., Perez-Alonso M., Obermaier B.,
Salanoubat M., LemcKe K., Rieger M., Perez-Alonso M., Obermaier B.,
Partmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
Delseny M., Boutry M., Artiguenave F., Robert C., Brottier P.,
Wincher P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Banger F.,
Wizedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Core eudicots; rosids;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
  Loreni F., Ruberti I., Bozzoni I., Pierandrei-Amaldi P., Amaldi F.; "Nucleotide sequence of the L1 ribosomal protein gene of Xenopus laevis: remarkable sequence homology among introns."; EMBO J. 4:3483-3488(1985).
                                                                                                     SEQUENCE OF 286-396 FROM N.A. MEDLINE=82262793; PubMed=7049839; Amaldi F., Beccari E., Bozzoni I., Luo Z.-X., Pierandrei-Amaldi P.; "Nucleotide sequences of cloned cDNA fragments specific for six "Nucleotide sequences of cloned cDNA fragments
                                                                                                                                                                                                                       -i- SIMILARITY: Belongs to the L4E family of ribosomal proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDLT -> LICA (IN REF. 2).
L -> P (IN REF. 2).
HAI -> MH (IN REF. 2).
R -> K (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
60S ribosomal protein L4-2 (L1).
RPL4B OR AT3G09630 OR F11F8.22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 406 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002136; Ribosomal L4/L1E.
Pfam; PF00573; Ribosomal L4; 1.
PROSITE; PS00939; RIBOSOMAL_L1E; 1.
                                                                                                                                                                                         Xenopus laevis ribosomal proteins.";
MEDLINE=86135987; PubMed=3841512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 321 L
337 339 HA
382 382 R
396 AA; 44906 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X05217; CAA28844.1; -. EMBL; V01438; CAA24699.1; -.
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                                                                                                                                                                                                                   17:311-316(1982).
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Q9SF40;
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CONFLICT
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RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J., RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D., RA Gooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D., RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E., Monfort A., Argiriou A., Flores M., Liguori R., Vitale D., Mewes H.-W., RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W., RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W., RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P., RA Rooney T., Rizzo M., Maiti R., Utterback T., Fujii C.Y., Shea T.P., RA Rooney T., Rizzo M., Maiti R., Utterback T., Fujii C.Y., Shea T.P., RA Fraser C.M., Nierman W.C., Salzberg S.L., White O., Venter J.C., RA Fraser C.M., Kaneko T., Nakamura Y., Salzberg S.L., White O., Venter J.C., RA Sasamoto S., Kimura T., Ideeawa K., Kawashima K., Kishida Y., Ra Nakayama S., Nakazaki N., Shinpo S., Takeuoh C., Mada T., Ra Matanabe A., Yamada M., Yasuda M., Tabata S., Muraki A., Shinpo S., Takeuchi C., Wada T., R. Haliana.", Sequence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAINLE.

STRAINLE.

STRAINLE.

MEDLINE=21016721; Pubbled=11130714; Kotani H., Kato T., Asamizu E., Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E., Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K., Kohara M., Matsumoto M., Muraki A., Nakayama S., Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T., Natanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M., Watanabe A., Yamada M., Sato S., A., Preston R., Huang E., Spiegel L., Gooj L., O'Shaughnessy A., Preston R., Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M., Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Batter M., Beller E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M., Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the L4E family of ribosomal proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      406 AA; 44702 MW; A56AFA6CEAF291F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60S ribosomal protein L4-1 (L1).
RPL4A OR RPL4 OR RPL1 OR AT5G02870 OR F9G14_180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P49691; Q9LXZ8;
01-FFBL-1996 (Rel. 33, Created)
28-FFBL-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AC016661; AAF23293.1; -. InterPro; IPR002136; Ribosomal_L4/L1E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE, PS00939; RIBOSOWAL L1E; 1.
Ribosomal protein.
SEQUENCE 406 AA: 44700 MM. RETAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85./*
Best Local Similarity 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 PRVPGGG 88
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                          Fulton R., Wohldmann P.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the L4E family of ribosomal proteins.

    -!- SIMILARITY: Belongs to the L4E family of ribosomal proteins.

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Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
NCBI_TaxID=6431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.3%; Score 33; DB 1; Length 386; 85.7%; Pred. No. 96; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.3%; Score 33; DB 1; Length 345; 85.7%; Pred. No. 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosenthal E.T.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS00939; RIBOSOWAL L1E; 1.
Ribosomal protein.
SEQUENCE 386 AA; 43135 MW; 23811EBEF015DD99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 AA; 38659 MW; C798B9DB0CED60AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Created)
01-FFB-1996 (Rel. 37, Last sequence update)
10-PBC-1998 (Rel. 37, Last annotation update)
60s ribosomal protein L4 (L1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                 Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                      EMBL; AF000196; AAC24253.1; -.
PIR; T34031, T34031, T34031, T34031, T34031, T8014.4; CE07669.
InterPro; IPR002136; Ribosomal_L4/L1E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, U30495; AAA74021.1; -.
PIR, T12048; T12048.
InterPro, IPR002136; Ribosomal_L4/L1E.
                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00573; Ribosomal L4; 1.
PROSITE; PS00939; RIBOSOMAL_L1E; 1.
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hes 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribosomal protein.
                                       NCBI_TaxID=6239;
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MEDLINE=86135987; PubMed=3841512;
Loreni F., Ruberti I., Bozzoni I., Pierandrei-Amaldi P., Amaldi F.;
"Nucleotide sequence of the L1 ribosomal protein gene of Xenopus
laevis: remarkable sequence homology among introns.";
EMBO J. 4:3483-3488(1985).
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Renopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the L4E family of ribosomal proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.3%; Score 33; DB 1; Length 396; 85.7%; Pred. No. 98; 1; Indels rative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAA29796).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P -> L (IN REF. 1; CAA29796)
P -> A (IN REF. 1; CAA29796)
; 2DA0FB693A1186BC CRC64;
                                                                                                                                                                                                                                                  P084<u>7</u>59; Q91843;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
6-CCT-2001 (Rel. 40, Last annotation update)
60S ribosomal protein L4A (L1A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
10-DEC-1998 (Rel. 37, Last annotation update)
60S ribosomal protein L4B (L1B) (Fragment).
                                                                                                                                                                                                                       396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002136; Ribosomal_L4/L1E.
Pfam; PF00573; Ribosomal_L4; 1.
PROSITE; PS00939; RIBOSOMAL_L1E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kenopus laevis (African clawed frog).
                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 AA; 44935 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X05216; CAA28843.1; -. EMBL; X06552; CAA29796.1; -. PIR; A24579; R5XL1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pram,
PROSITE; PSUUS...
Ribosomal protein.
1926
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                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 PRVRGGG 87
                                                            76 PRVRGGG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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2 PRVTGGG 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                        RPL4A OR RPL1A.
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                                                                                                                                                                                         RL4A XENLA
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SEQUENCE FROM N.A.

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REPUBLINE-2238257; PubMed-12477932.

REPUBLINE-2238257; PubMed-12477932.

REPUBLINE-2238257; PubMed-12477932.

REPUBLINE-2238257; PubMed-12477932.

REPUBLINE-2238257; PubMed-12477932.

REPUBLINE-2238257; PubMed-12477932.

REPUBLINE-238257; PubMed-12477932.

REPUBLINE-238257; PubMed-12477932.

REPUBLINE-238257; PubMed-12477932.

REPUBLINE-238257; PubMed-12477932.

REPUBLINE-238257; PubMed-12477932.

REPUBLINE-238257; Republic R. Branch A. R. Schaefer C.F., Bhat N.K., Antalen C.M., Hong L., Rapeton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rapeton M., Modin N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Richards S., Worley K.C., Shevchenko Y., Bouffard G.G., RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., McKay D.M., Sodewaten E.D., Dickson M.C., Shevchenko Y., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., "Generation and initial analysis of more than 15,000 full-length F. Thuman and mouse cDNA sequences";

R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16803(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89174988; PubMed-2494194; Saunders S., Jalkanen M., O'Farrell S., Bernfield M.; "Molecular cloning of syndecan, an integral membrane proteoglycan."; J. Cell Biol. 108:1547-1556(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BALB/c; TISSUB=Liver;
MEDLINE=93266605; PubMed=8496192;
Hinkes M.T., Goldberger O., Neumann P., Kokenyeji R., Bernfield M.;
"Organization and promoter activity of the mouse syndecan-1 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular polymorphism of the syndecans. Identification of a hypoglycanated murine syndecan-1 splice variant.";
J. Biol. Chem. 274:18667-18674(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Romaris M., Coomans C., Ceulemans H., Bruystens A.-M., Vekemans S.,
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vihinen T., Auvinen P., Alanen-Kurki L., Jalkanen M.; "Structural organization and genomic sequence of mouse syndecan-1
                                                                                                                                                   SDC1_MOUSE STANDARD; PRT; 311 AA. P18826; 062278; OSWTD2; PUNOV-1990 (Rel. 16, Leat sequence update) 01-NOV-1990 (Rel. 16, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) SDC1 OR SYND1 OR SYND1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 268:17261-17269(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99303636; PubMed=10373479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=93352511; PubMed=8349612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 2).
STRAIN=NMRI; TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Mammary gland;
MEDLINE=89174988; Publ
                                            240 PRTTGGAA 247
                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
2 PRVTGGGA 9
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           David G.
                                                                                                                                  SDC1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
N-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
CLEAVAGE OF ECTODOMAIN (POTENTIAL).
         -!- FUNCTION: Cell surface proteoglycan that bears both heparan sulfate and chondroitin sulfate and that links the cytoskeleton to the interstitial matrix.
-!-, SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prosite; ps00964; SYNDECAN; 1. Transmembrane; Glycoprotein; Signal; Proteoglycan; Heparan Bulfate; Transmembrane; Glycoprotein; Signal; Alternative splicing.
SIGNAL 1 17 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                            Note=Minor isoform;
-!- SIMILARITY: Belongs to the syndecan proteoglycan family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 1; Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 AA; 32904 MW; 283FEC396FF40FCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          007542
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                                                                                                                                                               IsoId=P18828-2; Sequence=VSP_007542;
                                                                                                        Name=1;
IsoId=P18828-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYNDECAN-1
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Biol. Chem. 268:11440-11448(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003585; Neurexin-like.
InterPro; IPR001050; Syndecan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seq.
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                             EMBL; XIS487; CAA33514.1; -.
EMBL; Z22532; CAA80254.1; -.
EMBL; AF134897; ADA4245.1; -.
EMBL; BC010560; AAA110560.1; -.
EMBL; L11565; AAA40159.1; -.
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01034; Syndecan; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                    Note=Major isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S06619; S06619.
MGD; MGI:1349162; Sdc1.
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                                                                                                                                                                                                        ö
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ignatovich O., Cooper M., Kulesza H.M., Beggs J.D.; "Cloning and characterisation of the gene encoding the ribosomal protein S5 (also known as rp14, S2, YS8) of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE-92184799; PubMed-1544921;
Takakura H., Tsunasawa S., Miyagi M., Warner J.R.;
"NH2-terminal acetylation of ribosomal proteins of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       !- SIMILARITY: Belongs to the S7P family of ribosomal proteins
                                                                                                                                                                                                      ;
                                                                                                                                                                  62.3%; Score 33; DB 1; Length 223; 85.7%; Pred, No. 55; 1; Indels iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
ROSE M., Koetter. P., Entian K.D.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                   223 AA; 25257 MW; F87541F6CEC26D74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1992 (Rel. 23, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
RPSS OR YUR123W OR J2045.
                                                                                                                                                                                                                                                                                                                                                         224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 23:4616-4619(1995).
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InterPro; IPR000235; Ribosomal_S7.
InterPro; IPR005716; Ribosomal_S7e/a.
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ProDom; PD000817; Ribosomal S7; 1.
TIGRPAMS; TIGR01028; S7_S5_EA; 1.
                                                               PDB; 1KG0; 27-MAR-02.
InterPro; 1PR001304; Lectin_C.
SMART; SW00034; CLECT; 1.
Hypothetical protein; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=96103590; PubMed=8524651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X89368; CAA61550.1; -.
EMBL; Z49623; CAA89654.1; -.
PIR; S55720; S55720.
PDB; IK5X; 22-MAY-02.
                               EMBL; V01555; CAA24860.1; -. PIR; F43042; QQBE26.
                                                                                                                                                                  Query Match
Best Local Similarity 85.73
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GermOnline; 141956; -.
                                                                                                                                                                                                                                                                       29 PRVRGGG 35
                                                                                                                                                                                                                                        2 PRVTGGG 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cerevisiae.
                                                                                                                                                                                                                                                                                                                                                         RSS YEAST
                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                         RESULT 20
RS5_YEAST
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                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteolytic pathway.
-!- SUBUNIT: The proteasome is composed of at least 15 non identical subunits which form a highly ordered ring-shaped structure (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARILY).
-!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
-!- SIMILARITY: Belongs to peptidase family T1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Proteasome subunit alpha type I (EC 3.4.25.1) (Proteasome subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Involved in an ATP/ubiquitin-dependent non-lysosomal
                                                                                                                                                                                                                                                                  0,
PROSITE; PS00052; RIBOSOMAL_S7; 1.
Ribosomal protein; Acetylation; Phosphorylation; 3D-structure.
                                                                                                                                                                                                  Score 33; DB 1; Length 224;
Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00227; proteasome; 1.
PROSITE; PS00388; PROTEASOME A; 1.
Proteasome; Hydrolase; Protease; Threcnine protease.
SEQUENCE 260 AA; 28311 MW; DREEFFSE480F8F70 CRC64;
                                                                               1 1 ACETYLATION.
20 20 T -> E (IN REF. 3).
224 AA: 24907 MW; A1354B6766981417 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 62.3%; Score 33; DB Best Local Similarity 75.0%; Pred. No. 64; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AR036694; AABBB344.1; -
PIR; T32525; T32525.
HSSP; P40302; IRYP.
MEROPS; T01.976; -
MOTTOPEP; CD4.6; CE16954.
InterPro; IPR000426; Pept T1_gubA.
InterPro; IPR001353; Peptidase_T1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                     62.3%;
                                                                                                                                                                    Query.Match
Best Local Similarity 77.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                145 TTRVGGGGA 153
                                                                                                                                                                                                                                                                                                                      1 TPRVTGGGA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAS-6 OR CD4.6
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044156;
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MEDLINE=98255987; PubMed=9654230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Cole S.T., Biglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Seeger K., Stalton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Mpetiphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECTES=M.tuberrulosis; STRAIN=CDC 1551 / Oshkosh; MEDLINE=22206494; PubMed=12218036; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
SIMILARITY: COAT PROTEINS FROM CARMOVIRUSES (CARMY, MNSV, TCV), DIANTHOVIRUSES (RCNMV), SOBEMOVIRUSES (MCMV, SBMV), TOMBUSVIRUSES (AMCV, CNV, CYRSV, AND TBSV), AND TNV ARE RELATED IN THEIR S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corymebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN, INTERACTION WITH RNA. DOMAIN, VIRION SHELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 1; Length 380; Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last amotation update)
Hypothetical PPE-family protein Rv2892C/MT2959/MD2916c.
RV2892C OR WT2959 OR MTCK274.23C OR MB2916C.
Mycobacterium tuberculosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     793CB6B05CEC6669 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PROJECTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                       HSSP; P11795; ZTBV.
InterPro; IPR008975; Viral_cap_coat.
InterPro; IPR008975; Viral_coat.
Pfam; PF00729; Viral_coat.
PRINTS; PR00233; ICOSAHEDRAL.
PROSITE; PS00555; ICOSAHEUR.COAT_S; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN,
DOMAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         380 AA; 40878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete genome sequence.";
                                                                                                                                                                                                                                       EMBL; M25270; AAA42904.1; -. PIR; JA0131; VCVGCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 393:537-544 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.0
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 TPSISGGGTI 327
                                                                                                                                                                                                                                                                                                                                                                                                                    254
380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 Coat protein.
DOMAIN
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                                                                  REGION
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                MEDLINE=22709107; PubMed=12788972;
MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grodini S., Lacroix C., Monsempe C., Simon S., Parvis B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; The complete genome sequence of Mycobacterium boyis.";

Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

-: SIMILARITY: Belongs to the mycobacterial PPE family.
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDIINE=04270667; PubMed=6087149;
MEDIINE=04270667; PubMed=6087149;
MEDIINE=04270667; PubMed=6087149;
Gibson T.G., Farrell P.G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٥;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 1; Length 408;
Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tluk; misso,
Tuberculist; Rv2892c; -.
InterPro; IRR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3E3D1F20D7827199 CRC64;
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Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Hypothetical BZLF2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                          Bacteriol. 184:5479-5490(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE007119; AAK47285.1; -. EMBL; BX248344; CAD96603.1; -. PIR; G70925; G70925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequ
10-OCT-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            408 AA; 41469 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.2%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 SPSVAGGGAV 301
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                                                                                     laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR; MT2959;
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                                                                                                                      Glaser P., Frangeul L., Buchriseer C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
A charbit A., Checouani F., Couve B., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Bntian K.-D., Faihi H., Garcia-del Portillo F., Garrido P.,
A Jones L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
A Jones L. M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Remmel B., Rose M., Schlueter T., Simose N., Tierrez A.,
Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
Comparative genomics of Listeria species.",
Science 294:88452[2011].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01099; HYETHIZKNASE.
TIGREAMs; TIGR00694; thim; 1.
Thiamine biosynthesis; Transferase; Kinase; ATP-binding; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: ATP + 4-methyl-5-(2-hydroxyethyl)-thiazole ADP + 4-methyl-5-(2-phosphoethyl)-thiazole. COFACTOR: Binds 2 magnesium ions per subunit (By similarity). PATHWAY: Thiamine blosynthesis. SIMILARITY: Belongs to the Thz kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Hydroxyethylthiazole kinase (EC 2.7.1.50) (4-methyl-5-beta-hydroxyethylthiazole kinase) (Thz kinase) (TH kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.2%; Score 34; DB 1; Length 269; 55.6%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAGNESIUM 1 (BY SIMILARITY).
MAGNESIUM 1 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7288ABFD23A760A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF_00228; -; 1.
InterPro; IPR000417; Hyethyz_kinase.
Pfam; PF02110; HK; 1.
                                                                          SEQUENCE FROM N.A.
STRAIN=CLIP 11262 / Serovar 6a;
MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 123 MA
269 AA; 28166 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL596164; CAC95574.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 55.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ListiList; LIN00341; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listeria monocytogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 PRITGSGCL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 PRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; AF1475; AF1475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1639;
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  Listeria innocua
                                    NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SITE
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   MEDLINE=2157279; PubMed=11679669;
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Charkraborty T.,
Charbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Bntian K.-D., Feihi H., Garcia-del Portillo F., Garrido P.,
Adutier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Neuster G.,
Androusen B., Matcourna A., Mata Vicente J., Nog E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simos N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
Comparative genomics of Listeria species.";
Science 294:849-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rochon D.M., Tremaine J.H.; "Complete nucleotide sequence of the cucumber necrosis virus genome."; Virology 169:251-259(1989).
-i- SUBGUNIT: THE VIRUS COAT IS COMPOSED OF 180 COPIES OF THE COAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cucumber necrosis virus (CNV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Tombusviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thiamine blosynthesis; Transferase; Kinase; ATP-binding; Magnesium; Complete proteome.
ACT_SITE 194 194 RACF / DV CIMITALITY.
                                                                                                                                                                                                                                                                64.2%; Score 34; DB 1; Length 269; 55.6%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE (BY SIMILARITY).
MAGNESIUM 1 (BY SIMILARITY)
MAGNESIUM 1 (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74A32D672176242C CRC64;
                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the Thz kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380 AA.
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, ALS91974; CADO0843.1; -.
PIR, AE1114; AE1114.
ListLinist, LMO00316; -.
LHAMP, MF 00228; -; 1.
LINEEPEO, IPRO00417; Hyethyz_Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-89204896; PubMed=2705296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01099; HYETHTZKNASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 123 M
269 AA; 28052 MW;
STRAIN=EGD-e / Serovar 1/2a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91
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SEQUENCE
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PROTEIN.

us-10-697-055-7.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Robb L. Hartley L. Wang C.-C. Harvey R.P., Begley C.G.;

Robb L. Hartley L. Wang C.-C. Harvey R.P., Begley C.G.;

Twisculin: a murine basic helix-loop-helix transcription factor gene expressed in embryonic skeletal muscle.";

McGr. Dev. 76:197-201(1998).

L. McGr. Dev. 76:197-201(1998).

-!- FUNCTION: Transcription repressor capable of inhibiting the transactivation capability of E47. May play a role in regulating antigen-dependent B-cell differentiation.

-!- SUBURIT: Efficient DNA binding requires dimerization with another bhill protein. Binds DNA as a homodimer or a heterodimer. Forms a heterodimer with E12/E47.

-!- SUBCELIULAR LOCATION Nuclear.

-!- TISSUE SEPECIFICITY: Expressed in lymphoid tissues, B-cell lines and activated B cells.

-!- SIMILARITY: Contains 1 basic helix-loop-helix (bHIR) domain.
      Attachberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Ridusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Ridusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Diatchenko L., Matusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Uodin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Uodin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Rha S.S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,
Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Raleseley R.W., Tucchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
T. Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50808; HLH; 1.
Transcription regulation; Repressor; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 603628; --
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0003714; F:transcription co-repressor activity; TAS.
GO; GO:0003708; F:transcription factor activity; TAS.
GO; GO:000366; F:transcription from Pol II promoter; TAS.
InterPro; IRR01092; HIM basic.
Pfam; PF00010; HIM; 1.
SWART; SM00363; HIM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> G (IN REF. 3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF060154; AAC15071.1; ALT_FRAME.
EMBL; BC006313; AAH06313.1; -.
EMBL; AF087036; AAC69870.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-GLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98440284; PubMed=9767165;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 6-206 FROM N.A.
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85
91
91
119
160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48
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DOMAIN
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dermOnline; 141109; -.

SGD; S0003029; DUOL.

GO; GO:0000778; C:condensed nuclear chromosome kinetochore; IPI.

GO; GO:000519; C:spindle; IPI.

GO; GO:0005200; F:structural constituent of cytoskeleton; IPI.

GO; GO:0000210; P:mitotic spindle assembly (sensu Saccharomyces); IPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97377993; PubMed=9234674; Feuermann M., de Montigny J., Potier S., Souciet J.-L.; The characterization of two new clusters of duplicated genes suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae chromosomes.";
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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                                                                                 0
                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 27.5 kDa protein in PYCl-UBC2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hydroxyethylthiazole kinase (EC 2.7.1.50) (4-methyl-5-beta-hydroxyethylthiazole kinase) (Thz kinase) (TH kinase).
THIM OR LIN0341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.2%; Score 34; DB 1; Length 247; 75.0%; Pred. No. 40;
                                               64.2%; Score 34; DB 1; Length 206; 85.7%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 247 AA; 27473 MW; 787F8AF869E3C978 CRC64;
DSD -> ASA (IN REF. 1).
21066E02553EB80C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 AA.
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                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
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 189 191 Di
206 AA; 22067 MW;
                                                                                                                                                                                                                                                                         (Rel. 34, Created)
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nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                   Conservative
                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast 13:861-869(1997).
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                               Query Match
Best Local Similarity
6; Conserve
                                                                                                                                                    75 PRVAGGG 81
                                                                                                                    2 PRVTGGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                         01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THIM LISIN Q92EW7;
                                                                                                                                                                                                                                                                                       01-OCT-1996
01-NOV-1997
                                                                                                                                                                                                                                         YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
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 CONFLICT
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                                                                                                                                                                                                                         YGG1_YEAST
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us-10-697-055-7.rsp

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TISSUE=Muscle;
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SEQUENCE FROW N.A.

STRAIN=CV. Columbia,

MEDLINE=21016719; PubMed=11130712;

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Alonso V., Chen H., Cheuk R.F., Chin C.W.,

Buehler E., Chan A., Coop D., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Croway A.B., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Fornsy T.H., Dewar K.,

Ann P., Etgu P., Feldblyum T.V., Feng J.-D., Hujzar L.,

Ann C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Ann C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Inn X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

An intischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

Rakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

An H., Tallon L.J., Tambunga G., Toriumi, M.J., Town C.D.,

Whu D., Yu G., Fraser C.M., Verbers J.C., Davis R.W.;

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22598051; PubMed=12679534;
Heim M.A., Jakoby M., Werber M., Martin C., Weisshaar B., Bailey P.C.;
"The basic helix-loop-helix transcription factor family in plants: a
genome-wide study of profin structure and functional diversity.";
Mol. Biol. Evol. 20:735-747(2003).
-!- FUNCTION: Transcription factor acting positively in the
                                                                                                                                                                                                                                                                                                                                                                                    SCRAIN-cv. Columbia;
Schoenbolm C., Weisshaar B.;
"Overview of the bHIH transcription factor gene family in Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Columbia;
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
"Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ni M., Tepperman J.M., Quail P.H.; "Binding of phytochrome B to its nuclear signalling partner PIF3 is reversibly induced by light."; Nature 400:781-784(1999).
                                                                                                                                                                                        SEQUENCE FROM N.A., STATES COLUMDIA. STATES. COLUMDIA. SONG P.-S., Choi G., ILE J., Yi H., Shin B., Song P.-S., Choi G., ILE J., Yi H., Shin B., Song P.-S., Choi G., Ildentification and characterization of three phytochrome-associated
       MEDLINE=99059501; PubMed=9845368;
Ni M., Tepperman J.M., Quail P.H.;
"PIF3, a phytochrome-interacting factor necessary for normal
photoinduced signal transduction, is a novel basic helix-loop-helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20259742; PubMed=10797009; Martinez-Garcia J.F., Huq E., Quail P.H.; Martinez-Garcia O.F., Huq E., Quail P.H.; "Direct targeting of light signals to a promoter element-bound transcription factor.";
                                                                                                                                                                                                                                                                                                          Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENE FAMILY ORGANIZATION, AND NOMENCLATURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99394605; PubMed=10466729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 288:859-863(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thaliana.";
Nature 408:816-820(2000).
                                                                                                                                         Cell 95:657-667(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thaliana.";
                                                                                                                                                                                                                                                                                                  proteins.
                                                                                                                    protein.
                     C RESERVED TO THE CONTROL OF THE CON
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                                To the G box (5'-CACGTG-3').

Subuntry: Homodimer (Probable). Can form a heterodimer with REP1.

Phytochrome B binds specifically to DNA-bound PIF3, but only upon red light induced conversion to the Pfr form (PfrB). Reconversion to Pr form causes rapid dissociation.

SUBCELLULAR LOCATION: Nuclear.

SUBCELLULAR LOCATION: Nuclear.

SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
phytochrome signaling pathway. Activates transcription by binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98252901; PubMed=9584154; Massari M.E., Rivera R.R., Voland J.R., Quong M.W., Breit T.M., van Dongen J.J.M., de Smit O., Murre C., "Characterization of ABF-1, a novel basic helix-loop-helix transcription factor expressed in activated B lymphocytes."; Mol. Cell. Biol. 18:3130-3139(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.0%; Score 35; DB 1; Length 524; 85.7%; Pred. No. 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR, 186228; H66228.
HS$P, P25312; 1HLO.
TRANSPAC; T04492; -
InterPro; IFR01092; HLH basic.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
PROSITE; PS5088; HLH; 1.
Nuclear protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E -> D (IN REF. 2).
S -> L (IN REF. 2).
1044AC01D598DE7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HELIX-LOOP-HELIX MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             060682; 075946; Q9BRE7;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 42, Last sequence update)
Musculin (Activated B-cell factor-1) (ABF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASIC DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-ARG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        524 AA; 56990 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phytochrome signaling pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 85.7%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356
393
358
428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSC OR ABF1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Page 10

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C STRAIN-CSTBL/61; IISSUE=Embryonic stem cells;

XX Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

XA Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S.,

A Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Alzawa K., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Alzawa K., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Alzawa K., Jashuli E., Bono H., Kandawa T., Saito R.,

XA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

XA Achim P., Lewis S., Matsuo Y., Nikaido I., Rochiwa H.,

Xa Sakai K., Okido T., Furuno M., Carninci P., Ga Bonaldo M.F.,

XA Sakai K., Bult C., Fletcher C., Fujita M., Gariboldi M.,

A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

A Brownstein M.J., Bult C., Recher C., Fujita M., Mombaerts P.,

A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Nordone P., Ring B., Kingwald M., Rodriguez I., Sakamoto N.,

A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

XA Wynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

A Wynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Schaefer C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Mang J., Heieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
B And S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Ratchieley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Bukesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note=No experimental confirmation available;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: High level of expression in liver, lung and testis. Also expressed in heart, brain, spleen, thymus and bone marrow. Highly expressed in progenitors and myeloid cells. Isoform 2 is expressed in primary hemotopoietic cells.
INDUCTION: Upregulated in the myeloid 32D cell line by granulocyte colony stimulating factor (G-CSF).
COMMAN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cellsurface receptor binding.
-:- DOMAIN: The BOX I motif is important for association with JAKS.
-:- SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 400:685-690(2001).

-!- FUNCTION: Receptor for thymic stromal lymphopoietin (TSLP). Forms a functional complex with TSLP and IL/7R which is capable of stimulating cell proliferation through activation of STAT3 and STAT5. Also activates JAK2. Implicated in the development of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hematopoietic system.
-!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1 and isoform 3). Secreted (isoform 2).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=08CII9-2; Sequence=VSP_008788, VSP_008789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q8CII9-3; Sequence=VSP_008790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=08CII9-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=2; Synonyms=Soluble CRLM-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 234-359 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             080555; QSSBC5; CREATED CREATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00060; FN3; 1.
PROSITE; PS01355; HEWATOPO REC_S_F1; FALSE_NEG.
Receptor; Signal; Transmembrane; Glycoprotein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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/FTId=VSP 008790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOKINE RECEPTOR-LIKE FACTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.0%; Score 35; DB 1; Length 359; 77.8%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 15 A -> T (IN REF. 1).
51 51 G -> S (IN REF. 4 AND 5).
87 87 A -> G (IN REF. 4).
179 179 A -> V (IN REF. 1 AND 3).
309 309 P -> T (IN REF. 1 AND 3).
359 AA; 37761 MW, F9C52LC54B4AG9DD CRC64;
-!- SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A -> G (in isoform 2).
/FTId=vSP 008788.
Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WSXWS motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                EMBL, AF201963, AAF82189.1; -. EMBL, BC023788, AAH23788.1; -. EMBL, AK010291; BAB26827.1; -.
                                                                                                                                                                                                                                          EMBL; AB039945; BAA92684.1; -. EMBL; AB031333; BAA92159.1; -.
                                                                                                                                                                                                                                                                   EMBL; AB03133; BAA92159.1; -. EMBL; AF232936; AAF81676.1; -.
                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1889506; TBlpr.
InterPro; IPR003961; FN III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 PRGPGGGAM 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
es 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254
1117
201
262
68
53
122
217
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G0:0046658; C:extrinsic to plasma membrane, GPI-anchored; ISS. G0:007050; P:cell cycle arrest; TAS. G0:0008285; P:negative regulation of cell proliferation; TAS. G0:0045749; P:negative regulation of S phase of mitotic c. .; NAS. wth arrest; GPI-anchor; Signal; Glycoprotein; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94173926; PubMed=8127893;
del Sal G., Collavin L., Ruaro M.E., Edomi P., Saccone S., Valle G.D.,
Schneider C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth-suppressing human homologue of the murine gasi gene.";
Proc. Natl. Acad. Sci. U.S.A. 91:1848-1852(1994).
-!- FUNCTION: Specific growth arrest protein involved in growth suppression. Blocks entry to S phase. Prevents cycling of normal and transformed cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GROWTH-ARREST-SPECIFIC PROTEIN 1. REMOVED IN MATURE FORM (POTENTIAL) POLY-ALA.
                                                                                                                                                                                                                                                                         ö
                                                                                                                                           BY SIMILARITY.
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                         66.0%; Score 35; DB 1; Length 321; 77.8%; Pred. No. 34;
                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                           / SIMILARITY.
DCSE39EF3CCD114C CRC64;
             Pfam; PF01341; Glyco_hydro_6; 1.
PRINTS; PR00733; GLHYDRLASES.
PRODOM; PD00373; GLYCOSYL HYDROL F6_1; FALSE_NEG.
PROSITE; PS00655; GLYCOSYL HYDROL F6_1; FALSE_NEG.
PROSITE; PS00656; GLYCOSYL HYDROL F6_2; 1.
Cellulose degradation; Hydrolase; Glycosidase; Signal.
27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure, function, and chromosome mapping of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Growth-arrest-specific protein 1 precursor (GAS-1).
                                                                                                                            ENDOGLUCANASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            345 AA
                                                                                                                                                                                                                                                                         0; Mismatches
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InterPro; IPR001524; Glyco_hydro_6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND FUNCTION.
                                                                                                                                                                                                          33694 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L13698; AAA72368.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Growth arrest; GPI-anchor;
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:4165; GAS1.
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318
345
91
                                                                                                                                           110
149
295
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                                                                                                                                                                                                                                                                                                             1 TPRVTGGGA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                            321 AA;
                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                             110
149
295
112
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P54826;
                                                                                                                                             ACT_SITE
ACT_SITE
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DISULPID
                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                              GAS1 HUMAN
                                                                                                                               CHAIN
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QBCII9, Q9CRJ6; Q9JIB7; Q9JJH8; Q9JMD5;
QBCII9, Q9CRJ6; Q9JIB7; Q9JIQ7; Q9JJH8; Q9JMD5;
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cytokine receptor-like factor 2 precursor (Type I cytokine receptor-like factor 2 precursor (Type I cytokine receptor)
delta 1) (Cytokine receptor-like molecule-2) (CRLM-2) (Thymic stromal lymphopoietin protein receptor) (TSLPR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning of a novel type I cytokine receptor similar to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Lymphocytes;
MEDLINE=20197866; PubMed=10733486;
Pujio K., Nosaka T., Kojima T., Kawashima T., Yahata T.,
Copeland N.G., Gilbert D.J., Jenkins N.A., Yamamoto K., Nishimura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=CS7BL/6; TISSUE=Lymphocytes;
MEDLINE=20432254; PubMed=10974032;
Park L.S., Martin U., Garka K., Gliniak B., Di Santo J.P., Muller W.,
Largaespada D.A., Copeland N.G., Jenkins N.A., Farr A.G.,
Ziegler S.F., Morrissey P.J., Paxton R., Sims J.E.;
"Cloning of the murine thymic stromal lymphopoietin (TSLP) receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning and characterization of CRLM-2, a novel type I cytokine receptor preferentially expressed in hematopoietic cells."; Biochem. Biophys. Res. Commun. 272:224-229(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Formation Of a functional heteromeric complex requires interleukin 7
                                                                                                                                                                                                                                                          Gaps
                                                                            GPI-anchor amidated serine (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pandey A., Ozaki K., Baumann H., Levin S.D., Puel A., Farr A.G., Ziegler S.F., Leonard W.J., Lodish H.F.; "Cloning of a receptor subunit required for signaling by thymic stromal lymphopoietin.";
                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hiroyama T., Iwama A., Morita Y., Nakamura Y., Shibuya A.,
                                                                                                                                                                                             DB 1; Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1), AND ALTERNATIVE SPLICING
                                                                                                             N-LINKED (GLCNAC. . .) (PC 2AAD50F1D3632F9D CRC64;
                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                              Pred. No. 36;
                                                                                                                                                                                                Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                           POLY-GLY
                                                         POLY-LEU
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MEDLINE=21177258; PubMed=10881176;
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                                                                                                                                               35721 MW;
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                                                                                                                                                                                                   66.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 common gamma chain.";
Blood 95:2204-2211(2000).
                                                                                                                                                                       Query Match
Best Local Similarity 75.v.
288
322
341
318
                                                                                                                                                                                                                                                                                                                                                                              148 PRTSGGGA 155
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285
319
337
318
117
                                                                                                                                                                                                                                                                                                                       2 PRVTGGGA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakauchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kitamura T.;
                                                                                                                   CARBOHYD
SEQUENCE
DOMAIN
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coved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Expression of branching enzyme II of maize endosperm in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
linkages in glycogen by scission of a 1,4-alpha-11,need
oligosaccharide from growing alpha-1,4-glucan chains and the
subsequent attachment of the oligosaccharide to the alpha-1,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   position.
CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHARY: Starch biosynthesis; third step.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Chloroplast; amyloplast.
-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11,4-alpha-glucan branching enzyme IIB, Chloroplast precursor (EC 2.4.1.18) (Starch branching enzyme IIB) (Q-enzyme).
                                                                                                                                                                                                                                                                                    67.9%; Score 36; DB 1; Length 295;
66.7%; Pred. No. 20;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 248-271 AND 305-315.
STRAIN=cv. B73; TISSUE=Endosperm;
MEDLINE=95152344; PubMed=7849565;
                                                                           EMBL; AE012186; AAM40186.1; -.
HARAPP, MF 00061; -; 1.
InterPro; IPR06204; GHMP_Kinase.
InterPro; IPR004424; IspE.
Pfam; PF00288; GHMP_Kinases; 1.
TIGRPAMS; TIGR00154; IspE; 1.
Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                295 AA; 31085 MW; 18F318EEA2FAD384 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fisher D.K., Boyer C.D., Hannah L.C.; "Starch branching enzyme II from maize endosperm."; Plant Physiol. 102:1045-1046(1993).
                                                                                                                                                                                                                                  ATP (POTENTIAL)
     modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 58-65.
STRAIN=CV. W64A X 182E; TISSUE=Endosperm;
MEDLINE=94105320; PubMed=8278524;
                       entities requires a license agreement (St
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Biol. 40:981-988(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guan H.P., Baba T., Preiss J.;
                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                       242 rPRLTGSGS 250
                                                                                                                                                                                                                                                                                                                                                                 1 TPRVTGGGA 9
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                    Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLGB MAIZE
                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                      BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLGB MAIZE
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                                                                                                  R InterPro; IPR006047; Alpha_amyl_cat.

R InterPro; IPR006047; Alpha_amyl_cat.

R InterPro; IPR00129; Glyco_hydro_13N.

R InterPro; IPR00129; alpha-amylase; 1.

R Ffam; PF02922; isoawylase; 1.

R Ffam; PF02922; isoawylase; 1.

R Glycogen biosynthesis; Starch biosynthesis; Transferase;

W Glycogen biosynthesis; Starch biosynthesis; Transft peptide.

FT ACT_SITE 1 57 CHOROPLAST (AMYLOPLAST).

FT ACT_SITE 341 341 BY SIMILARITY.

FT ACT_SITE 445 445 BY SIMILARITY.

FT ACT_SITE 445 447 BY SIMILARITY.

FT ACT_SITE 502 502 BY SIMILARITY.

FT ACT_SITE 502 502 BY SIMILARITY.

FT ACT_SITE 503 569 BY SIMILARITY.

FT ACT_SITE 504 569 BY SIMILARITY.

FT ACT_SITE 507 570 BY SIMILARITY.

FT ACT_SITE 507 570 BY SIMILARITY.

FT ACT_SITE 508 569 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CAUTION: It is uncertain whether Met-1 or Met-9 is the initiator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucans.-!- SIMILARITY: Belongs to cellulase family B (family 6 of glycosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Endoglucanase 1 precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase 1)
(Cellulase I) (CMCASE I) (CEL1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fernandez-Abalos J.M., Sanchez P., Coll-Fresno P.M.,
Villanueva J.R., Perez P., Santamaria R.I.;
"Cloning and nucleotide sequence of cellAl, and
endo-beta-1,4-glucanase-encoding gene from Streptomyces halstedii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 174:6368-6376(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 1; Length 799;
Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0B440E0377B8087A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 28-33.
STRAIN=JM8 / CECT3310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=JM8 / CECT3310;
MEDLINE=93015685; PubMed=1400190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90517 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.9%;
                           EMBL; L08065; AAA18571.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces halstedii.
                                                             T02981; T02981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 PRLTGGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    799 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 PRVTGGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELLOBIOSE.
                                                                                               MaizeDB; 63943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydrolases)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
ACT_SITE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P33682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GUN1_STRHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTHER PROCESS OF THE PROPERTY OF THE PARTHER PROPERTY OF THE PARTHER PROPERTY OF THE PARTHER PROPERTY OF THE PARTHER PARTHER PROPERTY OF THE PARTHER PARTHER
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EMBL; Z12157; CAA78145.1; -. HSSP; P26222; 1TML.

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(See http://www.isb-sib.ch/announce/
                                                                                                              pfam; PP00288; GHMP_kinases; 1.
TICRFAMS; TICR00154; ispE; 1.
Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                   67.9%; Score 36; DB 1; 66.7%; Pred. No. 20;
                                                                                                                                                                                 ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the ispE family.
                                                                                                                                                                                                                                                                      2; Mismatches
               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xanthomonas campestris (pv. campestris).
   entities requires a license agreement
                                                                HAMAP; MF 00061; -; 1.
InterPro; IPR006204; GHMP kinase.
InterPro; IPR004424; ISPE.
                                                 EMBL; AE011725; AAM35836.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 417:459-463(2002).
                                                                                                                                                                                                                                                   Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   methyl-D-erythritol.
                                                                                                                                                                                                                                                                                                                                       242 TPRLTGSGS 250
                                                                                                                                                                                                                                                                                                      1 TPRVTGGGA 9
                                                                                                                                                                    Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bimilarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=340;
                                                                                                                                                                                                                                                                                                                                                                                                                        ISPE XANCP
Q8PC64;
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                    BIND
                                                                                                                                                                                                                                                                                                                                                                                                        ISPE_XANCP
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=2002145; PubMed=12024217;

RA MEDLINE=22022145; PubMed=12024217;

RA Guaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Guaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Fornighieri E.F., Franco M.C., Ferreira R.C.C., Ferro M.I.T.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Machado M.A., Madeira A.M.B.N., Mayaki C.Y., Moon D.H.,

RA Mortins E.C., Matdanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Sctubal J.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

RA Sctubal J.C., Kitajima J.P.,

RA Sctubal J.C., Kitajima J.P.,

RA Sctubal J.C., Kitajima J.P.,

RA Nord Specificities, "...

RA Nord Specificities, "...

RA Nord Specificities, "...

RA Sctubal J.C., Kitajima J.P.,

RA Nord Specificities, "...

RA Nord Specificities, "...
                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol Kinase (EC 2.7.1.148) (CMK)
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol Kinase).

    -i- FUNCTION: Catalyzes the phosphorylation of the position 2 hydroxy
group of 4-diphosphocytidyl-2C-methyl-D-erythritol (By

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                          .,
                                                                                                                                                                                                                       Score 36; DB 1; Length 254; Pred. No. 17;
                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                        7424D7D1339A5F27 CRC64;

    -!- SIMILARITY: Belongs to the ispE family.

                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 295 AA.
                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                      PROTEIN GLIF.
                                                                         BMBL; Aboura...
PIR, 525281.
BCGGene; EG11514; gltF.
Signal; Transmembrane; Complete proteome.
1 25 POTENTIAL.
   send an email to license@isb-sib.ch)
                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas axonopodis (pv. citri).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
06 / ATCC 13902 / XV 101;
                                                                      EMBL; AE000401; AAC76246.1; -.
                                                                                                                                                                                        254 AA; 26351 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                         67.9%;
87.5%;
                                      EMBL; M74162; AAA23909.1; -.
                                                                                                                                                                                                         Query Match
Best Local Similarity 8/...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 417:459-463(2002).
                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                         AAA58016.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISPE OR IPK OR XAC0948.
                                                                                                                                                                                                                                                                                                                           45 TPVVTGGG 52
                                                                                                                                                                                                                                                                                          1 TPRVTGGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=92829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
                                                                                                                                                                                                                                                                                                                                                                                                              ISPE XANAC
                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            OBPNU1;
                                                                                                                                                                                                                                                                                                                                                                                            SPE_XANAC
                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                             STITE BREEFERS
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RX SILVABNICE FROM N.A.

RX MEDLINE=22022145; PubMed=12024217;

RX MEDLINE=22022145; PubMed=12024217;

RA Gasjlor R.B., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quagglor R.B., Monterior-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Quagglor R.B., Contavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Ciaracelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Actia J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katauyama A.M., Kishi L.T., Leite R.M. B.N., Martinez-Rossi N.M.,

Locali B.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Olivedira M.C., Oliveira V.R.,

RA Moreira L.M., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Frindade dos Santos M., Truffi D., Teai S.M., White F.F.,

RY Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,

RY Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,

RY Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,

RY Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,

RY Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,

RY Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,

RY Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,

RY Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,

RY Trindade dos Santos M. Truffi D., Teai S.M., White F.F.,

RY Nost Specificities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148) (CMK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: Catalyzes the phosphorylation of the position 2 hydroxy group of 4-diphosphocytidyl-2C-methyl-D-erythritol (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                        .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase).
ISPE OR IPK OR XCC0871.
                                                                                                                         Length 295;
                                                                                                                                                                                                                                  1; Indels
295 AA; 31057 MW; 9123D196F554A873 CRC64;
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                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disulfide bond (By similarity).
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF ITS C-TERMINUS (BY SIMILARITY).
-!- SIMILARITY: Belongs to peptidase family S1.
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heterodimer of two chains, light and heavy, held by a
            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAX SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "MOJECULAR Cloning and expression of rat prostasin.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Possesses a trypsin-like cleavage specificity (By
                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0722; CHYMOTRYPEIN.
SMART; SM00020; Tryp_SPC; 1.
SMOSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00134; TRYPSIN BER; 1.
Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein;
                                                                                                                                                                           Score 39; DB 1; Length 342; Pred. No. 6.5;
                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Kidney;
Adachi M., Kitamura K., Miyoshi T., Tomita K.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
INTERCHAIN (BY SIMILARITY).
                                                                                                                                               0620DE88ED187D0F CRC64;
                                                                                                                                                                                                                                                                                                                                                           Q9ESB7; Q9ER01;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                             342 AA
                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IRR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase SI.
InterPro; IPR001314; Peptidase_SIA.
                                                                                                                                                                                                                                                                                                                                                                                                                     Prostasin precursor (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB017638; BAB20281.1; -. EMBL; AF202076; AAG32641.1; -.
                                                                                                                                                  36729 MW;
                                                                                                                                                                              73.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                              Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                             244
2223
262
262
134
134
110
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                                                                                                                                                                                                                                        2 PRVTGGGA 9
37 11
168 2
201 2
234 2
85 134 1
134 1
159 3
342 AA;
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                                            DISULFID
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ACT_SITE
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CARBOHYD
CARBOHYD
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE=930/78627; PubMed=1447980;
MEDILINE=930/78627; PubMed=1447980;
Castano I., Flores N., Valle F., Covarrubias A.A., Bolivar F.;
"glrg, a member of the gltBDF operon of Escherichia coli, is involved
"in nitrogen-regulated gene expression.";
Mol. Microbiol. 6:2733-2741(1992).
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997)
-!- FUNCTION: INVOLVED IN INDUCTION OF THE SO-CALLED NTR ENZYMES IN RESPONSE TO NITROGEN DEPRIVATION, AS WELL AS IN GLUTAMATE BIOSYNTHESIS. MAY MEDIATE THE GLUTAMATE-DEPENDENT REPRESSION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAINSIZ 7. (MG1625.
STRAINSIZ 7. (MG16278503.)
Blattner F.R., Flunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Glasner H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                                                                                                                                                               (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
( POTENTIAL).
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Enterobacteriaceae; Escherichia.
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                     ACTIVATION PEPTIDE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                             73.6%; Score 39; DB 1; Length 342;
                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                             SERINE PROTEASE.
INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                     SED1AF05D9213B9B CRC64;
                                  PROSTATIN LIGHT CHAIN
PROSTATIN HEAVY CHAIN
                                                                                                                       BY SIMILARITY.
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(Rel. 24, Last sequence update)
(Rel. 40, Last annotation update)
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2; Mismatches
                                                                   SIMILARITY
            POTENTIAL.
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GLTF OR B3214.
                                                                                                                                                                                                                                                                                                                                                                                      43 PRITGGGS 50
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                                                                                                                                                                                                                                                                        342 AA;
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                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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37
70
168
201
234
85
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rangmembrane
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01-DEC-1992
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ID GLTF ECOLI
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CARBOHYD
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PSS8 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chee M.S. Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie B., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.; "Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.";

Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=87112940; PubMed=3027374; MEDLINE=87112940; PubMed=3027374; MEUGGER B., Klages S., Walla B., Albrecht J.-C., Fleckenstein B., Tomlinson P., Barrell B.G.; Primary structure and transcription of the genes coding for the two virion phosphoproteins pp65 and pp71 of human cytomegalovirus."; J. Virol. 61:446-453(1987).
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE=64272751; PubMed=6087357;
MEDILINE=64272751; PubMed=6087357;
Mande H., Baak S.W., Riggs A.D., Clark B.R., Shively J.E., Zaia J. Bande H., Baak S.W., Riggs A.D., Clark B.R., Shively J.E., Zaia J. Kilodaing and physical mapping of a gene fragment coding for a 64-kilodalton major late antigen of human cytomegalovirus.";
kilodalton major late antigen of human cytomegalovirus.";
co., Natl. Acad. Sci. U.S. A. 81.4965-4969(1984).
-!- FUNCTION: PORMS PART OF THE MATRIX OF THE HCMV VIRION.
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                                                                                              100.0%; Score 53; DB 1; Length 551; 100.0%; Pred. No. 0.026; cive 0; Mismatches 0; Indels
                                                          462 462 PHOSPHORYLATION.
551 AA; 61638 MW; C56D11AEB01F3C23 CRC64;
                                                                                                                                                                                                                                                                                                                                                  Human cytomegalovirus (strain AD169).
Viruses; daDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                                                                                                                                                                                                                                            01-JAN-1988 (Rel. 06, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
65 kDa lower matrix phosphoprotein (PP65).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR008649; Herpes UL82 83.
Pfam; PP05784; Herpes UL82 83; 1.
Matrix protein; Phosphorylation.
  EMBL; M67443; AAA45994.1; -.
InterPro; IPR008649; Herpes UL82_83.
Pfam; PF05744; Herpes UL82_83; 1.
MAITIX protein; Phosphorylation.
MOD_RES 462 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X17403; CAA35357.1; -.
EMBL; M15120; AAA45996.1; ALT_SEQ.
EMBL; K02531; AAA45983.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90269039; PubMed=2161319;
                                                                                                                             10; Conservative
                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                  407 TPRVTGGGAM 416
                                                                                                                                                        1 TPRVTGGGAM 10
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                                                                                                                Best_Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLETE GENOME.
                                                                                                                                                                                                                                                     PP65 HCMVA
P06725;
                                                                          SEQUENCE
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                                                                                                     Query Match
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                                                                                                                                Matches
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                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE=20235202; PubMed=10770960; Use of the property of the property N., Jaeger N.F., Pfister C., Bens M., Farman N., Courtois-Coutry N., Vandewalle A., Rossier B.C., Hummler B.: Activation of the amiloride-sensitive epithelial sodium channel by the serine protease mCAP1 expressed in a mouse cortical collecting duct cell line.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF ITS C-TERMINUS (BY SIMILARITY).
-!- SIMILARITY: Belongs to peptidase family $1.
-!- CAUTION: Ref.! sequence differs from that shown due to a frameshift in position 339.
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Am. Soc. Nephrol. 11:828-834 (2000).
-!- FUNCTION: Possesses a trypsin-like cleavage specificity (By similarity). Activates amiloride-sensitive sodium channels.
-!- SUBDNIT: Heterodimer of two chains, light and heavy, held by a disulfide bond (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Prostasin precursor (EC 3.4.21.-) (Channel activating protease 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRSSB OR CAPI.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVATION PEPTIDE (BY SIMILARITY). PROSTATIN LIGHT CHAIN. PROSTATIN HEAVY CHAIN.
                                                                                                                      0;
                                                     100.0%; Score 53; DB 1; Length 561; 100.0%; Pred. No. 0.027;
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                                                                                                                      0; Indels
62898 MW; 37422EA149E88F30 CRC64;
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INTERPRO; IPRODOBOOTS OF SET LTYPBIN.
INTERPRO; IPRODOLS4; Peptidase S1.
INTERPRO; IPRODOLS4; Peptidase S1A.
PRAM; PRODOLS9; LTYPBIN; 1.
PRINTS; PROOT22; CHYMOTRYPSIN.
SWART; SMOOZO, TTYP SPC; 1.
PROSITE; PSOOL34; TRYPSIN DOM; 1.
PROSITE; PSOOL35; TRYPSIN HIS; 1.
PROSITE; PSOOL35; TRYPSIN SIK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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HSSP; P00734; IUVS.
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                        Query Match
Best Local Similarity 100.'
Matches 10; Conservative
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MGD; MGI:1923810; Prss8.
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322
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286
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         561 AA;
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SIGNAL
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SERINE PROTEASE

1 KLF2 MOUSE Q60843	Q8eviit Q8ykg3	1 YMP4 STRCO	1 PLYB ASPNG Q00205	H :	1 ELIYA BACCS P41362	1 PLYA_COLGL Q00374	1 SUBN BACNA F33633	1 SUBT_BACST P29142	1 SUBT_BACSU P04189	1 KPBG HUMAN	1 KPBG RABIT FUUSTB	1 YGO7 WELLA O59002	1 IPOU DROME P24350	1 LEFI_MOUSE P27782		1 LEFT HUMAN OSKIDS	1 CTWD_RAT O9ers0	1 DEMA MOUSE	1 YAE1 SCHPO Q09842 schizosacc	1 DADA_XANAC Q8pgc9 xanthomona		THE PARTY OF THE P		ALIGNMENTS				STANDARD; PRT; 551 AA.		(Rel. 16, Created)	21, Last sequence update) 21 Tast sunctation undate)	(x phosphoprotein (PP64) (GP64).		Human cytomegalovirus (strain Towne). Winness, Ashna winness no Bha stage: Herpesviridae:	Betaherpesvirinae, Cytomegalovirus.			PubMed=1850902;	Pande H., Campo K., Tanamachi B., Zaia J.A.;	virus strain lowne ppos gene: nucleotide seguence Pschorichia coli ".	228 (1991) .		AND PHOSPHORYLATION.	Pubmed=zio/soi; Chirchill M.A., Zaia J.A.;	sis of a 64-kDa major structural protein of human	Towne): identification of a phosphorylation site and	comparison to pp65 of HCMV (AD169).";	(1990).	FUNCTION: FORMS FART OF THE ULB2 FAMILY.		This SWISS-PROT entry is copyright. It is produced through a collaboration	Actics and the bring outsides.	use by non-profit institutions as long as its content is in no way	statement is not removed. Usage by and for commercial	entities requires a license agreement (See http://www.lsb-slb.cn/announce/	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
	28 52.8 28 52.8																								_	•		CMVT	P18139;	-NOV-1990 (Rel.	-MAR-1992 (Rel.	kDa lower matr	UL83.	man cytomegalov	taherpesvirinae	NCBI TaxID=10363;	[1] POLIENCE EDOM N A	EDLINE=91220654;	ande H., Campo K	Human cytomegalo	irology 182:220-	5]	ARTIAL SEQUENCE,	EDLINE=9035//92; ande H 1.ee T F	Structural analy	ytomegalovirus (	omparison to ppe	irology 178:6-14	-!- FUNCTION: FOR		his SWISS-PROT e	between the Swith	ne suropean broi se by non-proi	odified and this	ntities required		
472	473	475	477	478	67.4	481	482	4 4 4 4 8 3 4 4 8 4 4 8 4 4 8 4 4 8 4 8	485	486	487	488	<b>4</b> 0 4 0 0 4	491	492	493	494	496	497	498	499	2006				1	RESULT I	10 01		DT																			99								
098vm8 arabidopsis	P56073 helicobacte	Q9jqv1 neisseria m	P34003 pseudomonas	Q87v14 pseudomonas	Q8zc15 yersinia pe	006235 mycobacteri	P43880 haemophilus	002732 sus scrota	Qecens scapmyrococ	P81130 scyliorhinu	P31740 xanthomonas	P72800 synechocyst	80	O15173 homo sapien	Q97ze2 sulfolobus	P78369 homo sapien	P37449 Balmonella	P14802 Dacilius Bu	DENIES DETECTION DE DENIES DE LA COMPANION DE	P41824 aplysia cal	O998g5 staphylococ	028706 archaeoglob	P73265 synechocyst	One 20 brassica na	Q46927 escherichia	P08419 sus scrofa	P49898 rana catesb	P29599 bacilius le	727	acil	CŢ.	Q9ce86 lactococcus	P38786 Baccharomyc	P00776 streptomyce	Q0049/ Iycopersico O929t7 bacillus ha	P52679 sphingobium	Q50665 mycobacteri	Passage Dacillus Bu	P24626 oryza Bativ	numan	1957/74 numan adeno	m sun	coxol	005826 gallue gall	nerne Pomo	5 4	P70353 mus musculu	rat	P47512 mycoplasma	meth	myco	mu.e	035602 mus musculu p15141 himan adeno	mus mu	thermu	ra	
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NOCCHLWAN
YGGI YEAST
THIM LISIN
YZLZ EBV
YS92_MYCTU
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YS92_MYCTU
YZLZ EBV
RS5_YEAST
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Maximum Match 100%
Listing first 500 summaries
                                                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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53
1 TPRVTGGGAM 10
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Perfect score:
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                                                                                                                              protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                           Run on:
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50878 rattus nor 36578 homo sapie	n Sini	escheric	drosophil	P23944 rattus norv O9.176 homo sanien	staphyloc	P54741 streptomyce p54742 strentomyce	rabidopsi	deinococc	nomo sap saccharo	Q876b4 saccharomyc	P40213 saccharomyc	Q09/34 trypamosoma Q8pjtl xanthomonas	046844 escherichia	O9hktl thermoplasm	000871 penaeus van	P36178 penaeus van	P49307 rhizobium m	P03185 epstein-bar	P10664 saccharomyc	P35679 schizosacch	Q9p784 schizosacch	Q8tuul methanopyru	Q9uzwu pyrococcus P50316 pyrococcus	O58965 pyrococcus	Q9z5x5 frankia sp.	Q03025 pseudomonas O10089 schizosacch	Q87gz9 vibrio para	Q19849 caenorhabdi p34809 crvnFococcii	P44779 haemophilus	Q95179 equus asinu b23388 r miltiphos	29ytr7 porcine ade	drosophila	PB1402 prunus pers O43017 prunus dulc	aeropyr	Q8/JZS Vibilo para 006114 mycobacteri	P95050 mycobacteri	P08088 pseudomonas	P34687 caenorhabdi	Q9i8j6 xenopus lae	arabid	psend	Q9wzv3 tnermotoga	P49669 trypanosoma	P32652 maize dwarf	092hpl rickettsia	listeria	listeria	Q9hi38 thermoplasm	treponema	Q9ugk8 homo sapien	vaniato vu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colinet D., Kummert J., Lepoivre P.;
"The nucleotide sequence and genome organization of the whitefly transmitted sweetpotato mild mottle virus: a close relationship with members of the family Potyviridae.";
Wirus Res. 53:187-196(1998).

EMBL: Z73124: CAA97466.1;
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sweet potato mild mottle virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MERCPE; CU6.001; -..

RECOPS; CU6.001928; C:viral capsid; IEA.

RG), GO:0005026; F:ATP binding; IEA.

RG); GO:0005026; F:ATP binding; IEA.

RG); GO:00040197; F:ATP dependent helicase activity; IEA.

RG); GO:00040197; F:Cysteine-type endopeptidase activity; IEA.

RG); GO:00040197; F:Cysteine-type endopeptidase activity; IEA.

RG); GO:0001676; F:Mud-circeted RNA polymerase activity; IEA.

RG); GO:0005198; F:Run-circeted RNA polymerase activity; IEA.

RINCEPPO; IRRO01369; Peptidase C6.

RINCEPPO; IRRO01369; RNA pol PSVir.

R Ffam; PRO0861; Peptidase C6; 1.

R Ffam; PRO0861; Peptidase C6; 1.

R Ffam; PRO0861; Peptidase C6; 1.

R Ffam; PRO0861; RNA dep RNA pol; 1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN.
W; C8D758543597C72A CRC64;
Best Local Similarity 77.8%; Pred. No. 1.4e+03; Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                          PRT; 3456 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A. MEDLINE=98281520; PubMed=9620210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3456 AA; 390279 MW;
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SMART; SMO0487; DEXDC; 1.
SMART; SMO0490; HELICC; 1.
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2181
3456
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                                                                                                                                                                             778 TPRATGRGA 786
                                                                                                             1 TPRVTGGGA 9
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2182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=41459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pomovirus.
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EXEMINECTERING. N.A.

SETAIN-CSTRENGE, TISSUB-Embryonic stem cells;

RA MEDLINE-21085660; PubMed=11217891;

RAMAN A. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

Arakawa T., Salabi K., Riyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Saito T., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Fleischmann W., Salubi F., Nikaido I., Pesole G., Quackenbush J.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Loon R.A.

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Myanbaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

A Wyanbaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Thymic stromal-derived lymphopoietin, receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 AA; 13321 MW; BD387D755A8D9DF6 CRC64;
                                                                      126 AA
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EMBL; AKO10291; BAB26827.1; -.
MGD; MGI:1889506; TSlpr.
                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.;
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RESULT 50
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67.9%; Score 36; DB 4; Length 1540;
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                                                                                                                                                                                                                                                                                                                                            2 PRVTGGGA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                            015080;
                                                                                                                                                                                                                                                                                                                                                                                                                               015080
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 48
                                                                                                                                                                                                                                                                                                                                                                                                                     015080
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                                                                                                                                                                                                                                                                                                                                                                                                        CTRAIN=TNSKZ;

A Pattery T. Bayese B., Beatson S., Geoffroy V., Meyer J.-M.,

A Pattery T., Bayese C., Martens J., Chablain P., Parsons Y.N.,

A Winstanley C., Cordwell S., Cornells P.,

"Identification of the two undescribed ferrippoverdine receptors from beudomonas aerudinosa.";

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF537095; AAN62913.1; --

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

RGO; GO:0004872; Fireapport ERA.

GO; GO:0004872; Fireapport activity; IEA.

GO; GO:0005215; Fireapport activity; IEA.

GO; GO:0006810; Pirransport: IEA.

RO; GO:0006810; Pirransport: IEA.

RO; GO:0006810; Pirransport: IEA.

RO; GO:0006811; Tonb boxC.

RIPRO0533; Tonb dep Rec; I.

RR Pfam; PP00533; Tonb dep Rec; I.

RR Pfam; PP00553; Tonb dep Rec; I.

RR Pfam; PP00553; Tonb dep Rec; I.
                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                               Gaps
                                                                                                                                                                                                                                                                                                                       Meyer J.M., Stintzi A., De Vos D., Cornelis P., Tappe R., Taraz K.,
                                                                                                                                                                                                                                                                                                                                     Budzikiewicz H.; "" " " type pseudomonads: the three Pseudomonas "Use of siderophores to type pseudomonas"."
                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 823;
      67.9%; Score 36; DB 2; Length 808; 75.0%; Pred. No. 7.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.9%; Score 36; DB 2; Length 823
Best Local Similarity 75.0%; Pred. No. 7.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels
                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q89UL2;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ATP-dependent protease ATP-binding subunit.
CLPB OR BLR1404.
                                                                                                                                                                01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 879 AA.
                                                                                                                                         823 AA
                                1; Mismatches
                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                             MEDLINE=97177770; PubMed=9025276;
                                                                                                                                                                                                                                                                                                                                                             aeruginosa pyoverdine systems.";
                                                                                                                                                                                                                                                                                                                                                                       Microbiology 143:35-43 (1997).
PRELIMINARY;
                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                            Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 TPGITGGG 198
                                                                       || :||||
176 TPGITGGG 183
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                                                        1 TPRVTGGG 8
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                   STRAIN=7NSK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                       FpvAII.
                                                                                                                                                       08GN89;
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                                                                                                                                           QBGNB9
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089UL2
089UL2
DC 089UL
DT 01-JU
DT 01-JU
DT 01-CPB
OS Barde
OC Brady
OX NCBI
RN [1]
RP SEQUE
                                                                                                                     RESULT 46
                                                                                                                                QBGN89
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Gaps
STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                     "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.9%; Score 36; DB 16; Length 879; 75.0%; Pred. No. 7.9e+02; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1540 AA; 163853 MW; 5CC4D2C8FE77083B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0F935D239D7A3867 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1990 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein KIAA0375 (Fragment).
                                                                                                                                                              Bradyrhizobium japonicum USDAIIO.";
DNA Res. 9:189-197(2002).
GNB APOSO24; F.ATP binding; IEA.
GO; GO:0005524; F.ATP binding; IEA.
GO; GO:0003754; F.chaperone activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
InterPro; IPR003595; AAAATPase centr.
InterPro; IPR001270; Chaprin CIpA/B.
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                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00004; AAA; 1.
Pfam; PF02861; CID N; 2.
PRINTS; PR00300; CLPPROTEASEA.
PROSITE; PS00870; CLPAB_1; 1.
PROSITE; PS00871; CLPAB_2; 1.
ATP-blag; Proteases; Complete proteome.
SEQUENCE 879 AA; 96621 MW; 0F935D239D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
MEDLINE=97349984; PubMed=9205841;
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InterPro; IPR001452; SH3.
Pfam; PF02759; RUN; 1.
Pfam; PF00018; SH3; 1.
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Best Local Similarity 75.v.
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SMART; SM00326; SH3; 1.
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Query Match
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Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                          Gaps
              Makasa S.B.;
"Analysis of the 3' terminal genomic region of sweet potato mild mottle virus isolates from Uganda.";
submitted (APR.2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ459318; CAD30642.1; -..
GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:001909; P:RNA-directed RNA polymerase activity; IEA.
InterPro; IPR001592; Poty_coat.
InterPro; IPR007094; RNA_pol_PSvir.
Fffm; PF00767; Poty_coat.
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                                                                                                                                                                     Length 501;
                                                                                                                                                             67.9%; Score 36; DB 12; Length 5U. 77.8%; Pred; No. 4.58+02; Lightles 1; Indels
                                                                                                                                                                                                                                                                                                                                                              Bacteria, Aquificae, Aquificales, Aquificaceae, Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       788 AA; 90804 MW; 3303E372FC719320 CRC64;
                                                                                                                          227 501 COAT PROTEIN.
1 226 NUCLEAR INCLUSION B.
501 AA; 57263 MW; DOCE93F71AD0B91A CRC64;
                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Lipoate-protein ligase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NULLE 392:353-358(1998).

EMBL; AE000748; AAC07512.1; -.

PIR, C70441; C70441.

GO; GO:0016874; F:11gase activity; IEA.

GO; GO:0006152; P:metabolism; IEA.

GO; GO:0006464; P:protein modification; IEA.

InterPro; IPR003704; CO dh/CoA synth.

Pfam; PF03099; BPL LipA LipB.

Pfam; PF03552; CO dh; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ligase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                  Local Similarity 77.8
Les 7; Conservative
                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                     269 PRVTGFGAL 277
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134 RITGGGAI 141
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                                                                                                                                                                                                                 2 PRVTGGGAM 10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       LPLA OR AQ 1638.
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                                                                                                                                                    SEQUENCE
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                                                                                                                                                                         Query Match
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O81387
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                                                                                                                                                                                                                                                                     RESULT 43
067557
                                                                                                                                                                                              Matches
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"Whole Genome Sequence Variation Among Multiple Isolates of Psedomonas
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Kim K.-N., Fisher D.K., Gao M., Guiltinan M.J.;

Wolecular cloning and characterization of the amylose-extender gene

"Molecular cloning and characterization of the amylose-extender gene

"Molecular cloning and characterization of the amylose extender gene

EMBL; AR072725; AAC33764.1; -.

EMBL; AR072725; AAC33764.1; -.

GO, GO.0005507; F.:alpha amylase activity; IEA.

GO, GO.0005507; F.:copper ion binding; IEA.

GO, GO.0005975; F.:carbohdrate metabolism; IEA.

GO, GO.0005975; P.:carbohdrate metabolism; IEA.

GO, GO.0006918; P.:elactron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
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Spencer D., Kab A., Smith B., Raymond C., Sims E., Hastings M.,
Burns J., Kaul R., Olson M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.9%; Score 36; DB 10; Length 799; 85.7%; Pred. No. 7.2e+02; ive 1; Mismatches 0; Indels
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Pfam; PF00593; TonB dep_Rec; 1.
SEQUENCE 808 AA; 89414 MW; 4C7972A4D310E25C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006647; Alpha amyl_cat.
InterPro; IPR006647; Alpha amyl_cat.
InterPro; IPR004193; Glyco hydro_l3N.
InterPro; IPR007110; Ig-like.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase N; 1.
PROSTIE; PS001096; COPPER BLUE; 1.
SEQUENCE 799 AA; 90665 MW; 4FD7B1EBC3B759F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) Starch branching enzyme IIb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF540992; AA017428.1; --
EMBL; AF540992; AA01743.1; --
EMBL; AF540993; AA01743.1; --
EMBL; AF540993; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transporter activity; IEA.
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17 PRLTGGG 23
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                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    NCBI_TaxID=4577;
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                                                                                                                                            Zea mays (Maize)
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=41459;
                                                           227
                                                                                                                                                                                                                                                                                                                                                                 STRAIN=RUK2;
                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ipomovirus
                                                                                                    Query Match
                                              NON TER
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                                                                    CHAIN
                                                                                                                                                                                                 RESULT 41
Q8B325
                                                                                                                         Matches
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                                              Gaps
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                                                                                                                                                                                                                  Sweet potato mild mottle virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                          Makasa S.B.;
"Analysis of the 3' terminal genomic region of sweet potato mild mottle virus isolates from Uganda.";
submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ459314; CAD30638.1; --
GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0019079; F:RNA-directed RNA polymerase activity; IEA.
InterPro; IPR0010592; Poty coat.
InterPro; IPR007094; RNA_pol PSvir.
Fam; PP00767; POCY_coat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mukasa S.B.;
Malyais of the 3' terminal genomic region of sweet potato mild motile virus isolates from Uganda.";
Submitted (APR-2002) to the BBEL/GenBank/DDBJ databases.
EMBL; AJ459115; CAD30639.1; --
GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
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                    67.9%; Score 36; DB 12; Length 501; 77.8%; Pred. No. 4.5e+02; tive 1; Mismatches 1; Indels
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501 AA; 57173 MW; 89DD08B244DBEC1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             1 226 NUCLEAR INCLUSION B.
501 AA; 57182 MW; FO6CD1D0061D3DB1 CRC64;
                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Coat protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UN3-2003 (TrEMBLrel. 24, Last annotation update)
Coat protein (Fragment).
                                                                                                                                             501 A.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sweet potato mild mottle virus.
                  Query Match
Best Local Similarity 77.8'
Matches 7; Conservative
                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                    269 PRVTGFGAL 277
                                                               2 PRVTGGGAM 10
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                                                                                                                                                                                                                                                   NCBI_TaxID=41459;
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                                                                                                                                                                                                                                           [pomovirus.
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                                                                                                                  RESULT 39
Q8B327
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Viruses; BSRNA positive-strand viruses, no DNA stage; Potyviridae;
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Pred. No. 4.5e+02;
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                                                                                                                                                                                                         1; Indels
                                                                                                            1 226 NUCLEAR INCLUSION B.
501 AA; 57371 MW; D2C1967FEIEF5A27 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                     Q8B325;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Coat protein (Fragment).
GO; GO:0019079; P:viral genome replication; IEA. InterPro; IPR001592; Poty_coat. InterPro; IPR007094; RNA_pol_PSvir. Pfam; PF00767; Poty_coat; 1.
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                                                                                                                                                              67.9%;
77.8%;
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Best Local Similarity 77.00,
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3 RVTGGGAM 10

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Q8B329
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the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taylor K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
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                                                                                Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkhill J., Bentley S.D., Barrell B.G., Rajandream M.A.; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                          Query Match 67.9%; Score 36; DB 10; Length 38 Best Local Similarity 75.0%; Pred. No. 3.5e+02; Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oliver K., Harris D.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
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GO; GO:000664, P:protein modification, IEA.
InterPro; IPRO04143; BPL_LipA_LipB.
Pfam; PF03099; BPL_LipA_LipB, 1.
Hypothetical proteIn; Complete proteome.
SEQUENCE 388 AA; 41814 MW; 9AAlDE930DF6FC4A CRC64;
                      383 AA; 40697 MW; D0336CA0423584CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TrEMBLrel: 07, Last sequence update) 01-OCT-2003 (TrEMBLrel: 25, Last annotation update) Mypothetical protein SC06423. SC06423 OR SC1A6.12C. Streptomyces coelicolor.
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                                                                                                                                                                                                                                                                                                                                                                              388 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                                                                                                                         214 TPRTSGGG 221
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Best Local Similarity
Thes 6; Conserva
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                                                                                                                                                                                    1 TPRVTGGG
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Gramene; Q9ARP7;
SEQUENCE 383 A
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Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mukasa S.B.;

Analysis of the 3' terminal genomic region of sweet potato mild mottle virus isolates from Uganda.";

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ459312; CAD30636_1;

EMBL; AJ459312; CAD30636_1;

EMBL; AJ459312; PRNA-directed RNA polymerase activity; IEA.

GO; GO:0019079; P:RNA-directed RNA polymerase activity; IEA.

InterPro; IPR001592; Poty_coat.

InterPro; IPR007094; RNA_pol_PSvir.

Pfam:

Pfam
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ459313; CAD30637.1; -.
GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:019079; P:viral genome replication; IEA.
InterPro; IPR001592; Poty_coat.
InterPro; IPR00767; RNA_Pol_Psvir.
Phan; PF00767; Poty_cat: 1.
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Pred. No. 4.5e+02;
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501 AA; 57249 MW; 77EF5647FB966A6C CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                           (TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                501 AA.
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                                                                                                                                                                                                                                                                                                                                                                     Sweet potato mild mottle virus.
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Best Local Similarity 77.00,
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205 RISGGGAM 212
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01-JUN-2003
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"The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract.";
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-NCC 2705;
MEDLINE=22294977; PubMed=12381787;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B., Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M., Pridmore R.D., Arigoni F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Actinobacteria, Actinobacteridae, Bifidobacteriales, Bifidobacteriaceae, Bifidobacterium.
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                                                  Score 36; DB 2; Length 354;
Pred. No. 3.2e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
       354 AA; 38074 MW; 4C7674E1F23741DD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).
EMBL; AB014748; AAN25024.1;
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0006464; P:protein modification; IEA.
InterPro; IPR004143; BPL Lipa Lipa.
Ffam; PF03099; BPL Lipa Lipa.
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Probable lipoate protein ligase.
SNOP OR BL1217.
                                                67.9%;
75.0%;
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es 7; Conservative
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OSJNBA0010K01.19.
                                                                                                        6; Conservative
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                                                                              Best Local Similarity
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SEQUENCE FROM N.A.
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       SEQUENCE
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Q8G501
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"A gene cluster involved in nogalamycin biosynthesis from Streptomyces nogalater: sequence analysis and complementation of early-blocked mutations in the anthracycline pathway.";

Mol. Gen. Genet. 251:113-120(1996).
                    Loessner M.J., Inman R.B., Lauer P., Calendar R., "Complete nucleotide sequence, molecular analysis and genome structure of bacteriophage Al18 of Listeria monocytogenes: implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 27451;
MEDLINE=96349102; PubMed=8760909;
Ylibonov K., Hakala J., Kunnari T., Mantsala P.;
Production of hybrid anthracycline antibiotics by heterologous expression of Streptomyces nogalamycin biosynthesis genes.";
Microbiology 142:1965-1972(1996).
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MEDLINE=98007868; PubMed=9349712;
Torkkell S., Yihonko K., Hakala J., Skurnik M., Mantsala P.;
Torkkell S., Yihonko K., Hakala J., Skurnik M., Mantsala P.;
"Characterization of Streptomyces nogalater genes encoding enzymes involved in glycosylation steps in nogalamycin biosynthesis.";
Mol. Gen. Genet. 256:203-209(1997).
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                                                                                                                                                                                                                                                                                            67.9%; Score 36; DB 9; Length 262; 87.5%; Pred. No. 2.4e+02;
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ224512; CAB59005.1; -.
                                                                                                                                                                                                                                              262 AA; 30217 MW; 11B66231BDB6F440 CRC64;
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GO; GO:0006464; P:protein modification; IEA.
InterPro; IPR004143; BPL_LipA_LipB.
PF03099; BPL_LipA_LipB; 1.
                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                  Mol. Microbiol. 35:324-340(2000).

EMBL; AJ242593; CAB53832.1; -.

GO; GO:0003677; F:DNA binding; IEA.

InterPro; IPR005039; Anti_rep.
MEDLINE=20117992; PubMed=10652093;
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01-OCT-2003
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MEDLINE=22608306; PubMed=12692562;
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:226-531(2003).
BMBL, AP005050; BA715291;
Hypothetical protein; COmplete proteome.
SEQUENCE 244 AA; 26824 MW; E953E6C988699ABD CRC64;
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                                                                                                                   MEDLINE=21477403; PubMed=115/2948; Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitiils: deducing the ability of producing secondary metabolites.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 16; Length 244; Pred. No. 2.2e+02;
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                                                                                SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
     Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
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70.0%;
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Matches 7; Conservative
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Rasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Rattei B., McIntosh T.C., McLeod M.P., McPherson D., A. Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Raleon D.L., Ra Reinard G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinard M., Stunders R.D.C., Scheeler F., Shen H., RA She B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Wellsen S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao G., Zhao X.H., Myers B.W., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., RA Glibbs R.A., Myers B.W., Rubin G.M., Venter J.C.; Radica C. Stience 287:2185-2195(2000)

R. Science 287:2185-2195(2000)

R. Fybsee, Februolosse, Call 1294, RSSP, PO6601; 1FJL.

R. Science 287:2185-2195(2000)

R. Fybsee, Februolosse, Call 1294, RSSP, PO6601; 1FJL.

R. Science 287:2185-2195(2000)

R. Fybsee, Februolosse, Call 1294, RSSP, PO6601; 1FJL.

R. Science 287:2185-2195(2000)
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SEQUENCE 261 AA; 28643 MW; 27A9BF152F372FF3 CRC64;
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GO: 00:0016491; F:oxidoreductase activity; IEA.
GO: 00:001370; F:transcription factor activity; IEA.
GO: 00:00152; P:metabolism; IEA.
GO: 00:006355; P:regulation of transcription, DNA-deg
InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR001356; Homeobox.
InterPro; IPR001366; Homeobox.
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SMART; SM00389; HOX; 1.
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B97, cv. CI187-2, cv. CML254, cv. CML258, cv. D940Y, cv. 1205, cv. IDS28, cv. IL101, cv. KI21, cv. KI3, cv. M162W, cv. MO17, cv. N28HT, cv. NC260, cv. NC348, cv. OH43, cv. PA91, cv. T232, cv. TX601, and cv.
                                                                                                                                                                                                                                                                                                                                                                                                        Whitt's.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler B.S. IV.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY235251; AAP03728-1; -
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                                                                              WI53R;
MEDLINE=22247734; PubMed=12244216;
MRDLINE=22247734; PubMed=12244216;
Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S.;
"Genetic diversity and selection in the maize starch pathway.";
"Genetic diversity and selection in the maize starch pathway.";
Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962(2002).
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Bradyrhizobium japonicum.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Bradyrhizobiaceae, Bradyrhizobium.
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EMBL; AY235277; AAP03753.1; -.
EMBL; AY235278; AAP03756.1; -.
EMBL, AY235279; AAP03756.1; -.
GO; GO:0005507; F:copper ion binding; IEA.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0006118; P:electron transport.
InterPro; IRRO0023; BlueCu 1.
PROSITE; PS00196; COPPER_BLUE; 1.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Blr6432 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AY235252; AAP03729.1; -.
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Best Local Similarity 85.77
Matches 6; Conservative
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EMBL; AY235275; P
EMBL; AY235276; P
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                                                         Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K., Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M., Tabata S.,
                                                                                                                    "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bardyrhiczobium japonicum USDA110.";
DNA FSE: 9:189-197(2002)
EMBL; AP005958; BAC51697.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21588047; PubMed=11731481; Hang J., Lih C.J., Pan K.H., Cohen S.N.; Hang J., Lih C.J., Pan K.H., Cohen S.N.; Hang J., Lih C.J., Pan K.H., Cohen S.N.; Ardlobal analysis of growth phase responsive gene expression and regulation of antibiotic biosynthetic pathways in Streptomyces coelicolor using DNA microarrays."; Emes Dev. 15:3183-3192(2001).

EMBL; AR42594; AAM78437.1; Godo, GO:0003824; F:catalytic activity; IEA.

GO: GO:0003824; F:catalytic activity; IEA.

HiterPro: IPR004143; BPL_LipA_LipB.

Pēms; PF03099; BPL_LipA_LipB. 1.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                67.9%; Score 36; DB 16; Length 181; 75.0%; Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                 1; Indels
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                1; Mismatches
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01-0CT-2002 (TrEMBLrel. 22, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
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                           STRAIN-USDA 110;
MEDLINE-22484998; PubMed-12597275;
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Best Local Similarity 75...
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70 PRIIGGGA 77
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SEQUENCE FROM N.A.
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STRAIN=CV. PI566691;
Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays subsp. mays (maize).
Zea mays subsp. yiridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                             Zea mays (subsp. parviglumis) (Balsas teosinte).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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STRAIN=cv. PI566691;
MEDLINE=22247734; PubMed=12244216;
Whitt S.N. Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S.;
"Genetic diversity and selection in the maize starch pathway.";
Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 139;
                                          Length 139;
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139 139 MW; 0D196F5F025F493B CRC64;
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GO; GO:0005489; F:copper ion binding; IEA.
GO; GO:0015489; F:clectron transporter activity; IEA.
GO; GO:00118; F:electron transport; IEA.
INTERPRO; IPR000923; BlucCu 1.
PROSITE; PS00196; COPPER BLUE; 1.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                             67.9%; Score 36; DB 10;
85.7%; Pred. No. 1.3e+02;
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Q84JQ6;
01-JUN-2003 (TEMBLrel. 24, Created)
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                                                               Best Local Similarity 85.7
Matches 6; Conservative
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STRAIN=cv. PI566689;
White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY232419; AA092759.1; -.
GO; GO:0005507; F:copper ion binding; IEA.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000923; BlueCu I.
PROSITE; PS00196; COPPER_BLÜE; 1.
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STRAIN—CV. DISF6686;
Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
BMBL, AY232418, AM03758-11,
GO, GO:0005507; F:copper ion binding; IEA.
GO, GO:0005489; F:electron transporter activity; IEA.
GO, GO:0005489; F:electron transport; IEA.
InterPro; IRR000923; Blucu 1.
PROSITE; PS00196; COPPER_BLÜE; 1.
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Ebkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoldeae; Andropogoneae; Zea.
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MEDLINE=22247734; PubMed=12244216;
Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler B.S.;
"Generic diversity and selection in the maize starch pathway.";
Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962(2002).
                                                                                                         Zea mays (subsp. parviglumis) (Balsas teosinte).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                   STRAIN=CV. PIS668;

MEDLINE=22247734; PubMed=12244216;

Mitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S.;

"Genetic diversity and selection in the maize starch pathway.";

Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962(2002).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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STRAIN=cv. IC-3;
White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY23446; AA092756.1; -.
GO; GO:0005507; F:copper ion binding; IEA.
GO; GO:0005499; F:electron transporter activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000923; BlucCu l.
PROSITE; PS00196; COPPER BIUE; 1.
Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S.; "Genetic diversity and selection in the maize starch pathway."; proc. Natl. Acad. Sci. U.S.A. 99:12959-12962(2002).
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Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; AX232415; AAO92755.1;
GO; GO:0005507; F:copper ion binding; IEA.
GO; GO:0005508; F:electron transporter activity; IEA.
GO; GO:000518; F:electron transport; IEA.
InterPro; IPR000923; BlueCu 1.
PROSITE; PS00196; COPPER_BLUE; 1.
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Bukaryota; Viridiplantae; Streptophyta; mbryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
PACCAD clade, Panicoideae, Andropogoneae, Zea.
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MEDLINE=22247734; PubMed=12244216;
WEDLINE=22247734; PubMed=12244216;
Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S.;
Whitt S.R., Wilson L.M., Tenaillon in the maize starch pathway.";
Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962(2002).
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85.7%; Pred. No. 1.3e+02;
ive 1; Mismatches 0; Indels
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                                139 AA; 14664 MW; 1E45805F024BDE83 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE=22247734; PubMed=12244216;
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                                                                              Query Match
Best Local Similarity 85./*
---- 6; Conservative
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17 PRLTGGG 23
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STRAIN=cv. P1331785;
White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY232417; AAO92757.1; -..
GO; GO:0005507; F:copper ion binding; IEA.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:00066118; P:electron transport; IEA.
InterPro; IPR000923; BlueCu_I.
PROSITE; PS00196; COPPER_BLÜE; 1.
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                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=cv. PI331785;
MADELINE=22247734, PubMed=12244216;
White E.S., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S.;
"Genetic diversity and selection in the maize starch pathway.";
"Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962 (2002).
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85.7%; Pred. No. 1.3e+02;
Live 1; Mismatches 0; Indels
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01JUN-2003 (TrEMBLrel. 24, Created)
01JUN-2003 (TrEMBLrel. 24, Last sequence update)
01JCT-2003 (TrEMBLrel. 25, Last annotation update)
Amylose extender 1 (Fragment).
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Q84QG1
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             STRAIN=cv. CML333;
White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AV235261; AAP03738.1; -initing, IEA.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
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MEDLINE=22247734; PubMed=12244216;
Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler B.S.;
Whitt S.R., Wilson L.M., also selection in the maize starch pathway.";
"Genetic diversity and selection in the maize starch pathway.";
Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962(2002).
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Pred. No. 1.3e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                   67.9%; Score 36; DB 2; Length 127; 66.7%; Pred. No. 1.2e+02; tive 1; Mismatches 2; Indels
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PROSITE; PS00196; COPPER_BLUE; 1.
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85.78;
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17 PRLTGGG 23
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Q84QG2;
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STRAIN=cv. F2;
White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY235264; AAP03741.1; -..
GO; GO:0005507; F:copper ion binding; IEA.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
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Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S. IV.;
Submitted (FEB-2003) to the BMBL/GenBank/DDBJ databases.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                               Zea mays subsp. mays (maize).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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MEDLINE=22247734; PubMed=12244216;
Whitt S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S.;
"Genetic diversity and selection in the maize starch pathway.";
Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962(2002).
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=2224734; PubMed=12244216; White S.R., Buckler E.S.; White S.R., Wilson L.M., Tenaillon M.I., Gaut B.S., Buckler E.S.; "Genetic diversity and selection in the maize starch pathway."; Proc. Natl. Acad. Sci. U.S.A. 99:12959-12962(2002).
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01-07N-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Amylose extender starch-branching enzyme (Fragment)
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Amylose extender starch-branching enzyme (Fragment)
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01-OCT-2003
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RESULT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531(2003).
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                                                                                                                                                                 MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=33903;
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                      SEQUENCE FROM N.A.
STRAIN-MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP005041; BAC72891.1; ... GO; GO:0009274; C:cell wall (sensu Bacteria); IEA. GO; GO:0003824; F:catalytic activity; IEA. GO; GO:0008658; F:penicillin binding; IEA. GO; GO:0009252; P:peptidoglycan biosynthesis; IEA.
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01-JUN-2003 (TrEMBLrel, 24, Last sequ
01-JUN-2003 (TrEMBLrel, 24, Last sunc
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Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Glyco_trans_51; 1.
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InterPro, IPR001460; Transpeptdse.
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Best Local Similarity 75.0'
Matches 6; Conservative
  Streptomyces avermitilis.
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SAV5477.
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Q82C77
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Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Rahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti pSymk megaplasmid.";
Phroc. Natl. Acad. Sci. U.S.A., 98:9883-9888 (2001).
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                Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                         "Complete genome sequence and comparative analysis of the industrial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RA0336 OR SMAGG38.
Rhizobium meliloti (Sinorhizobium meliloti).
Rhizobium meliloti (Sinorhizobium meliloti).
Badenid psymA (megaplasmid 1).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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Pred. No. 78;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                           Score 36; DB 16; Length 54;
Pred. No. 50;
3; Mismatches 1; Indels
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Hypothetical protein; Plasmid; Complete proteome.
SEQUENCE 85 AA; 9300 MW; 8C966E072243521C CRC64;
                                                                                                                                                                                  Hypothetical protein; Complete proteome.
SEQUENCE 54 AA; 5884 MW; 7FEIDFB025140016 CRC64;
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01-NOV-1996 (TYEMBLrel. 01, Last sequence update)
01-JUN-2003 (TYEMBLrel. 24, Last annotation update)
ORF2 frame shift at position 226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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NCBL_TaxID=1575;
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                                                                                                   microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
EMBL; AP005043; BAC73189.1; -.
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MEDLINE=22608306; PubMed=12692562;
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Best Local Similarity 60.0.
Best Local Similarity 60.0.
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                                                                                                                                                                                                                                                                                                                                                                          1 TPRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                            :|:||||:
28 SPYMTGGGAL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 TPSVIGGGA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TPRVTGGGA 9
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yeast one-hybrid system method.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY341856; AAQ20915.1;
SEQUENCE 379 AA; 39956 WW; B233AD060113C84D CRC64;
                                                                                                                                   339 PAVAGGGAM 347
                                                                                                            2 PRVTGGGAM 10
                                                                       Local Similarity
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SEQUENCE 653 AA
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"Isolation of rice WRKY protein through W-box bait vector by modified
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                      Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Bhrhartoideae, Oryzeae, Oryza.
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.8%; Score 37; DB 10; Length 379; 77.8%; Pred. No. 2.3e+02; tive 0; Mismatches 2; Indels
 69.8%; Score 37; DB 16; Length 345; 66.7%; Pred. No. 2.1e+02; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                clone:P0006C01.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002839; BAB19096.1; -.
EMBL; AP002844; BAB19095.1; -.
                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 15, Last annotation update)
Putative DNA-binding protein homolog.
P0688A04.2 OR P0006C01.17.
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GO; GO3677; F:DNA binding; IEA.
InterPro; IPR003657; WRKY.
Pfam; PP03106; WRKY; 1...
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les 7; Conservative
               Best Local Similarity 66.7
Matches 6; Conservative
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                                                                          192 PKLAGGGAM 200
                                                    2 PRVTGGGAM 10
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C STRAIN=ATCC 19089 / CB15;

STRAIN=ATCC 19089 PubMed=11259647;

A Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

A Bisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

B Detocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

A DeBOY R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

A Salzberg S.L., Venter J.C., Sappiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

R EMBL, ABC06598, AAK22239.1; --.
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Caulobacteraceae; Caulobacter.
NCBI_TaxID=155892;
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69.8%; Score 37; DB 10; Length 379; 77.8%; Pred. No. 2.3e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           653 AA; 70503 MW; 395D98388A3772DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Penicillin-binding protein, 1A family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0009274; C:cell wall (sensu Bacteria); IEA.
GO; GO:0008824; F:catalytic activity; IEA.
GO; GO:0008658; F:penicillin binding; IEA.
GO; GO:0009252; P:pepridoglycan biosynthesis; IEA.
InterPro; IPR001264; Glyco trans
                                                                                                                                                                                                                                                                                                                                                        653 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Glyco_trans_51; 1.
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Matches 9; Conservative
                                                                    7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caulobacter crescentus.
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WEDLINE-22827954; Pubmed=12910271;
WEDLINE-22827954; Pubmed=12910271;
WEDLINE-22827954; Pubmed=12910271;
WEDLINE-22827954; Pubmed=12910271;
WARTHIB U., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
WACHTIB U., Homele M., Temple L., James K., Harris B., Quail M.A.,
Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
Collingworth T., Collinm M., Cronin A., Davis P., Doggett U.,
W. Feltwell T., Goble A., Hamlin M., Hauser H., Holroyd S., Jagels K.,
Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
Rabbinowitsch B., Rutter S., Sanders D., Seeger K.,
Abbinowitsch B., Rutter S., Sanders M., Saunders D., Seeger K.,
Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
Comparative analysis of the genome sequences of Bordetella pertussis,
Bordetella parapertusis and Bordetella bronchiseptica.";
REBL: Bordetella parapertusis and Bordetella bronchiseptica.";
REBL: Bridetella Parapertusis and Bordetella bronchiseptica.";
REBL: Bridetella Parapertusis and Bordetella bronchiseptica.";
REBL: Bridetella Parapertusis.
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                                                         Bordetella parapertussis.
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Alcaligenaceae, Bordetella.
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Alcaligenaceae, Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 16; Length 25:
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
3 258 AA; 28296 MW; 2246BDF651E190AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28296 MW; 2246BDF651E190AF CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Putative lipoate-protein ligase A.
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01-00T-2003 (TrEMBLrel. 25, Last sequence update)
01-00T-2003 (TrEMBLrel. 25, Last annotation update)
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87.5%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=TOHAMA I / ATCC BAA-589 / NCTC 13251;
MEDLINE=22827954; PubMed=12910271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nat. Genet. 35:32-40(2003).
EMBL; BX640414; CAE41593.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.8%;
                                                                                                                                                                                 STRAIN=12822 / ATCC BAA-587;
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Best Local Similarity 87...
7, Conservative
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                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                       NCBI_TaxID=519;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Length 258;

Best Local Similarity

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Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
"The complete genome sequence of the carcinogenic bacterium
Helliobacter hepaticus.";

Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).

EMBL, AE017148; AAP78075.1;
                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                          MEDLINE=22825698; PubMed=12917642; Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P., Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M., Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A., Webb E.A., Zinser E.R., Chisholm S.W.;
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                                                                                                                                                                                                                                      Prochlorococcus marinus (strain MIT 9313).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 16; Length 264;
Pred. No. 1.6e+02;
1; Mismatches 1; Indels
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 264 AA; 28534 MW; 4E3D89A3750C51D0 CRC64;
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                                                                                                                                                                             Last sequence update)
Last annotation update)
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Last annotation update)
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Nature 424:1042-1047(2003).
EMBL, BX572101; CAR22321.1; -.
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 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Complete proteome. SEQUENCE 345 AA; 38138 MW; 05F9948CD
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                                                                                                                                                             (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last seqn
(TrEMBLrel. 25, Last anno
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MEDLINE=22709201; PubMed=12810954;
                                                                                                                                                                                                     Hypothetical protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.8%;
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(TrEMBLrel. 25,
(TrEMBLrel. 25,
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
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81 RVSGGGAM 88
                             3 RVTGGGAM 10
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                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                   Prochlorococcus.
NCBI_TaxID=74547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=32025;
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01-OCT-2003
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01-OCT-2003
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Matches
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                                                                                                      RESULT 9
                                                                                                                    27V426
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Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
Yamada K., Liu S.X., Sakano H.L., Toriumi M., Yu G., Bowser L.,
Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lawa B., Lin J.,
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.
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Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
Yamada C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F1511.14.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Columbia;
Vygotekaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Vygotekaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Lii J., Kremenetskaia I., Lurce J., Ngan i., Gonzalez A., Altafi H.,
Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Huizar L., Kim C., Palm C., Rowley D., Shinn P., Warker M.,
Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome I BAC F15I1 sequence.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; "Full-length messenger RNA sequences greatly improve genome
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
F1511.14 protein (Putative DNA-binding protein) (Hypothetical
                                                                                                                                                                                                                                         71.7%; Score 38; DB 11; Length 340;
85.7%; Pred. No. 1.48+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Theologis A.; "Full Length cDNA of gene F15I1.14 (GI:4587547)."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                          3C2540E9B3A81C8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
  InterPro; IPR001314; Peptidase SIA.
                         Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYSEN.
SMART; SM0020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
SEQUENCE 340 AA; 35503 MW; 3C25
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                                                                                                                                                                                                                                                                                                     6; Conservative
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                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                     2 PRVTGGG 8
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                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
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STRAIN=RB50 / ATCC BAA-588;

(X MEDLINE=22827954; PubMed=12910271;

(M REDLINE=22827954; PubMed=12910271;

(M REDLINE=22827954; PubMed=12910271;

(M REDLINE=22827954; PubMed=12910271;

(M Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

(A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

(M Achtman M., Aktin R., Baker S., Basham D., Bason N., Cherevach I.,

(A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

(A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

(A Rabinowitsch B., Norberczak H., O'Neil S., Ormond D., Price C.,

(A Rabinowitsch B., Rutter S., Sanders M., Squares R., Squares S., Stevens K.,

(A Rabinowitsch B., Wastlen J., Skelton J., Squares R., Squares S., Stevens K.,

(A Rabinowitsva analysis of the genome sequences of Bordetella pertussis,

(A Rabinowits S., Sharis S., Sanders B., Seelen S., Stevens K.,

(A Rabinowitsva analysis of the genome sequences of Bordetella pertussis,

(A Rabinowits S., Sharis S., Sharis S., Sharis S., Stevens K.,

(A Rabinowits S., Sharis S., S
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Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.8%; Score 37; DB 16; Length 258; 87.5%; Pred. No. 1.6e+02; ive 1; Mismatches 0; Indels
        Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.7%; Score 38; DB 10; Length 383; 87.5%; Pred. No. 1.5e+02; ative 0; Mismatches 1; Indels
                                                                                                               "Full-Length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006577; AAD25778.1; -.
EMBL; AF360325; AAKX6035.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica (Alcaligenes bronchisepticus)
                                                                                                                                                                                                                                                                                        EMBL, AY056333; AAL07182.1; -.
EMBL; AY084772; AAM61340.1; -.
PIR, C96881, C96581.
GO; GO:0003677; F:DNA binding; IEA.
Hypotherical protein; DNA-binding.
SEQUENCE 383 AA; 41731 MW; D7AE4D93DAF2BIEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 AA; 28296 MW; 2246BDF651E190AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTW618;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative lipoate-protein ligase A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 RVTGGGAM 10
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=518;
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Q7W618
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OBBJV6
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        Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                               .
0
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0
                                                                                                                                                                                                                                                                                                                                73.6%; Score 39; DB 11; Length 255; 75.0%; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                               0; Indels
        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                                                                                                                                                                                                                                    1F96A6EF2431FF73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2003 (TrEMBLrel. 25, Last amotation update)
Similar to protease, serine, 8 (Prostasin).
PRSS8.
                                                                                            Last sequence update)
Last annotation update)
  0.53;
                                                                                                                                                                                                                                                                                                                                                                                                              339 AA.
                                                                                                                                                                                                                                                                                                                                               2; Mismatches
        0; Mismatches
 Pred. No.
                                                                                     Created)
                                                                      PRT;
                                                                                                                                                                                                                                                                                      PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
SMSITE; PSS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
SEQUENCE 255 AA; 27355 WW; IFS
100.08;
                                                                             Q8C1L4;
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
        10; Conservative
                                                                       PRELIMINARY;
                                417 TPRVTGGGAM 426
                      1 TPRVTGGGAM 10
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43 PRITGGGS 50
                                                                                                                                                                                                                                                                                                                                                              2 PRVTGGGA 9
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                         NCBI TaxID=10090;
                                                                                                                                                                 STRAIN=C57BL/6J;
                                                                                                          Prostasin.
                                                                                                                                                                                                                                                                                                                                                                                                              Q99L44
                                                                        Q8C1L4
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
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                                                                Q8C1L4
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Eye;

MEDINE=22354683; PubMed=12466851;

The FANTOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II Team;

A malysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

Nature 420:563-573(2002).

REMEL, AKO76869; BAG27362.1; -.

REMEL, AKO76869; BAG27362.1; -.

ROJ, GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004289; F:trypsin activity; IEA.

ROJ, GO:0004289; F:trypsin activity; IEA.

ROJ, GO:0006289; P:proteolygis and peptidolysis; IEA.

ROJ, GO:0006289; P:proteolygis and peptidolysis; IEA.

ROJ, GO:0006289; P:proteolygis and peptidolysis; IEA.

RIHGEPPC; IPR009003; Cys Ser Irypsin.

RIHGEPC; IPR001254; Peptidase_51.
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SEQUENCE FROM N.A. STRAINSTRELLUNG: STRAINE-129/SvJ, and Swiss; TISSUE-Lung: STRAINE-129/SvJ, and Swiss; TISSUE-Lung: Caughey G.H.: Caughey G.H.: "Molecular cloning and characterization of mouse prostasin, a type I membrane-associated serine protease of the gamma-tryptase/prostasin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGC:1922810; Pras8.

RG; GO:0004263; F:chymotrypsin activity; IEA.

RG; GO:0004263; F:peptidase activity; IEA.

RG; GO:0004295; F:trypsin activity; IEA.

RG; GO:0004295; F:trypsin activity; IEA.

RG; GO:0006508; P:proteolysis and peptidolysis; IEA.

RILEFPRO; IPR001254; Peptidase_S1.

RILEFPRO; IPR001254; Peptidase_S1.

REARTHYS; PR001234; Peptidase_S1A.

RRART; SM00020; LYPPSIN 1.

RRART; SM00020; TYPPSIN DOM; 1.

RRART; SM00020; TYPPSIN DOM; 1.

RROSITE; PS00134; TRYPSIN HIS; 1.

RROSITE; PS00135; TRYPSIN HIS; 1.

RROSITE; PS00135; TRYPSIN JER; 1.

RHYDIOJASE; ROSIOS; RYPSIN JER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                "mouse serine protesse.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                     Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                     Kitamura K., Takefumi N., Kimio T.;
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC003851; AAH03851.1; -. EMBL; AF378086; AAL06320.1; -. EMBL; AF378085; AAL06319.1; -. EMBL; AB038244; BAB82496.1; -. HSSP; P00734; IUVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 PRITGGGS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 PRVTGGGA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=10090;
                                                                                                                                                                          gene family.
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Q9akx4 legionella Q8nd25 homo sapien O18487 penaeus van O7u368 pordetella Q7u368 bordetella Q7u368 bordetella Q7u368 bordetella Q8500 streptomyce Q66458 kepatitis c Q9eyi4 streptomyce Q87pzl vibrio para Q4382 agrobacteri Q9ayza bacteriopha Q9852 brucella me Q8tyd brucella me Q9148 prachaena sp Q9145 pra rhadino Q9145 pra rhadino Q9144 pra rhadino Q9148 streptomyce Q8x68 streptomyce Q8x68 streptomyce Q8x68 streptomyce Q8x16 vibrio vuln Q8110 vibrio para	ridae; ridae; brary and screening of databases.
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APPLICANT:

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| Sequence 730, Application US/10102806
| Publication No. US20030054421A1
| SERERAL INFORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE OF INVENTION: NUMBER: US/10/102,806
| CURRENT FILING DATE: 2002-03-22 |
| PRIOR PELICATION NUMBER: 09/925,298 |
| PRIOR PELICATION NUMBER: 09/925,298 |
| PRIOR PELICATION NUMBER: PCT/US00/05881 |
| PRIOR PELICATION NUMBER: PCT/US00/05881 |
| PRIOR PELICATION NUMBER: 60/124,270 |
| PRIOR PERIOR PE
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64.2%; Score 34; DB 9; Length 263;
Best Local Similarity 75.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                            APPLICANI: IKEDA, MASATO
APPLICANI: IKEDA, MASATO
APPLICANI: OZAKI, AKIO
ITITE OF INVENTION: NOVEL POLYNUCLEOTIDES
TITLE REPRENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159163
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER: PATENTION NUMBER: JP 00/280988
SQ ID NO 4695
LENGTHAL: 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 r TYPE: PRT corynebacterium glutamicum US-09-738-626-4695
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-10-102-806-730
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86 RMSGGGAM 93
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US-10-102-806-730
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Gaps
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                                                                                                                                                                                ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 3282941CD1
US-10-247-671-173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION WOMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PLING DATE: 2000-04-07
PRIOR PLING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4633, Application US/09738626
Publication No. US2020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 4695, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Corynebacterium glutamicum
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
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ANDO, SEIKO
       PRIOR FILING DATE: 2001-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
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SOFTWARE: Patentin ver. 3.0
SEQ ID NO 4633
LENGTH: 260
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Best Local Similarity 85./*
Si Conservative
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OCHIAI, KEIKO
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                         NUMBER OF SEQ ID NOS: 186
SOFTWARE: PERL Program
                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                      SEQ ID NO 173
LENGTH: 206
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APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Canada and their use in the modification of plant development
FILE REFERENCE: 11000.1022c1
CURRENT PERIOR DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR APLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR PLILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 262
LENGTH: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
GURRENT APPLICATION NUMBER: US/10/369,493
GURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
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                                                                                                                                                                                                                                                                                                                                                                                        64.2%; Score 34; DB 14; Length 128; 75.0%; Pred. No. 2.3e+02; rive 1; Mismatches 1; Indels
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APPLICANT: Shiffman, Dov
APPLICANT: Porter, Gordon, J.
APPLICANT: Raser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
FILE REFERENCE: PA.0050 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/247,671
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/323,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17800, Application US/10369493; Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 173, Application US/10247671
Publication No. US20030194721A1
GENERAL INFORMATION:
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Best Local Similarity 75.v.
Loca 6; Conservative
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SEQ ID NO 17800
LENGTH: 148
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                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Pinus radiata
US-10-219-220-262
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ORGANISM: SPHINGOMONAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PRVTGGGA 9
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Gaps

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Sequence 71, Application US/10219220
; Sequence 71, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
APPLICANT: Flinn, Barry
; TILE OF INVENTION: Compositions affecting programmed cell
; TILE OF INVENTION: Composition affecting programmed cell
; TILE OF INVENTION WIMBER: US/10/219,220
; CURRENT FILING DATE: 1099-106-04
; PRIOR FILING DATE: 1099-106-04
; NUMBER OF SEQ ID NOS: 290
; SEQ ID NOS: 290
; SEQ ID NO 71
: LENGTH: 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.2%; Score 34; DB 14; Length 86; 75.0%; Pred. No. 1.6e+02; tive 1; Mismatches 1; Indels
          Length 524;
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TITLE OF INVENTION: No. US20040005560Alel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT PILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
                                                         0. Indels
       Score 35; DB 14;
Pred. No. 6.4e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; sequence 2675, Application US/10108260A; Publication No. US20040005560A1 ; GENERAL INFORMATION:
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             Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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Matches 6; Conservative
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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US-10-219-220-262
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2003-02-28
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6241
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                                                                                                                                          Query Match
Best Local Similarity 70.0%; Pred. No. 6.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels
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APPLICANT: STOPETHAND, JAMES
APPLICANT: STOPETHAND, JAMES
APPLICANT: STOPETHAND, JAMES
TITLE OF INVENTION: A UNIVERSAL LIGHT-SWITCHABLE GENE
TITLE OF INVENTION: PROMOTER SYSTEM
TITLE OF INVENTION: PROMOTER SYSTEM
CURRENT APPLICATION NUMBER: US 60/355,402
PRIOR APPLICATION NUMBER: US 60/355,402
PRIOR FILING DATE: 2002-08-06
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 11
SOFTARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                    US-10-369-493-6241
; Sequence 6241, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Caenorhabditis elegans
                                                 TYPE: PRT; ORGANISM: Caenorhabditis elegans US-10-369-493-6240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Quail, Peter H. APPLICANT: Hug, Enamul
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LENGTH: 524
; SEQ ID NO 6240
; LENGTH: 522
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Sequence 6240, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Gao, Yongwei

APPLICANT: Glater, Steven C.

APPLICANT: Gladman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFEINS IN PLANTS FOR PRODUCTION OF;

TITLE OF INVENTION: EXPRESSION OF MICROBIAL BROYED PROPERTIES

TITLE OF INVENTION: USABLES US/10/369,493

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT PILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey,
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REPERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
SUTMERN OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 66.0%; Score 35; DB 14; Length 444; Best Local Similarity 66.7%; Pred. No. 5.4e+02; Matches 6; Conservative 0; Mismatches 3; Indels
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
LENGTH: 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7677, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Candida albicans
US-10-032-585-7677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 PRAAGGGVM 381
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US-10-369-493-6240
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LENGTH: 502
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US-10-314-657-23

Sequence 23, Application US/10314657

Sequence 23, Application No. US20030175888A1

Sequence 23, Application No. US20030175888A1

Sequence 23, Application No. US20030175888A1

Sequence 23, Application No. US2003017588A1

SEQUENCE INFORMATION:

APPLICANT: CHENG, Yi-Ciang

APPLICANT: CHENG, Yi-Ciang

APPLICANT: TANG, Gong-Li

TITLE OF INVENTION: Synthases and Methods of Use

FILE REPERENCE: 054030-0021

CURRENT APPLICATION NUMBER: PCT/US02/08937

FRIOR APPLICATION NUMBER: PCT/US02/08937

FRIOR APPLICATION NUMBER: PCT/US02-02-05

FRIOR APPLICATION NUMBER: US 60/278,935

FRIOR APPLICATION NUMBER: 201-03-26

NUMBER OF ESQ ID NOS: 214

SOFTWARE: PatentIn version 3.2

SEQ ID NO 23

SEQ ID NO 23

LENGTH: 432
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                          APPLICANT: Schading, Richard L.
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
TITLE OF INVENTION: RESISTANCE
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                                                                                                      FILE REFERENCE: 218.29/203 (EBG-003)
CURRENT APPLICATION NUMBER: US/10/441,736
CURRENT FILING DATE: 2003-05-20
FRIOR APPLICATION NUMBER: 60/107,243
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver: 2.1
SOFTWARE: 424
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; APPLICANT: SHIBA, TADAYOSHI; APPLICANT: SHIBA, TADAYOSHI; APPLICANT: SAKAKI, YOSHIKUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Streptomyces atroolivaceus
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Pseudomonas syringae
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Best Local Similarity 66.7°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                APPLICANT: Wei, Zhong-Min
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1 TPRVTGGGA 9
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US-09-879-248-14
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Sequence 9, Application US/09835684

Sequence 9, Application US/09835684

Sequence 102202019337A1

GENERAL INFORMATION:

APPLICANT: Wei, Zhong-Min

APPLICANT: Remick, Dean

TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR

TITLE OF INVENTION: DESICCATION

TITLE OF INVENTION: DESICCATION

CURRENT APPLICATION NUMBER: US/09/835,684

CURRENT APPLICATION NUMBER: 60/198,359

PRIOR PILING DATE: 2000-04-19

NUMBER OF SEQ ID NOS: 12
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Patent No. US200200596581
GENERAL INFORMATION:
APPLICANT: Wei, Zhong-Min
APPLICANT: DeRocher, Jay
TITLE OF INVENTION: METHODS OF IMPROVING THE EFFECTIVENESS OF TRANSGENIC
TITLE OF INVENTION: METHODS
FILE REPERENCE: 21829/91
CURRENT APPLICATION NUMBER: US/09/880,371
CURRENT FILING DATE: 2001-06-13
FRIOR FILING DATE: 2000-06-15
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                                                                                       Score 35; DB 9; Length 370;
Pred. No. 4.58+02;
0; Mismatches 2; Indels
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US-09-880-371-9
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                                                                                             66.0%;
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 424
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Best Local Similarity 66.7.
The Conservative
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Best Local Similarity 77.8-
Best Local Similarity 77.8-
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                                                                                                                                                                                                          344 PRGPGGGAM 352
                        TYPE: PRT
CORGANISM: Mus musculus
US-09-895-593-2
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       LENGIH: 370
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Sequence 14. Application US/09879248

Patent No. US2002062500A1

GENERAL INFORMATION:
APPLICANT: Fan, Hao
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT FILING DATE: 2001-06-12

PRIOR APPLICATION NUMBER: 60/212,211

PRIOR FILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 14
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US-10-441-736-14
Sequence 14, Application US/10441736
Publication No. US20040016029A1
GENERAL INFORMATION:
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169 rPTATGGGS 177
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Matches 6; Conserva
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APPLICANT: Baumann, Heinz
APPLICANT: Levin, Steven D.
APPLICANT: Farr, Andrew G.
APPLICANT: Leonard, Warren J.
APPLICANT: Loonard, Warren J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Lodish, Harvey F.
APPLICANT: Lodish, Harvey F.
APPLICANT: Uses Thereof
FILE REFERENCE: 00-514-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SATISTANDER Chris
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and
TITLE OF INVENTION: Uses Thereof
FILE REPERENCE: 00-514-C
CURRENT PAPLICATION NUMBER: US/09/895,943
CURRENT PILING DATE: 2001-06-28
PRIOR PAPLICATION NUMBER: 60/214,866
PRIOR APPLICATION NUMBER: 60/214,866
NUMBER OF SEQ 1D NOS: 16
SOFTWARE: PATENTING DATE: 2001-06-28
NUMBER OF SEQ 1D NOS: 16
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Pred. No. 4.4e+02;
1; Mismatches 1; Indels
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CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: 60/215,658
CURRENT APPLICATION NUMBER: US/10/226,872 CURRENT FILING DATE: 2002-12-05 NUMBER OF SEQ ID NOS: 33 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09895943; Patent No. US20020068323A1; GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
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Best Local Similarity 75.v.
Lee 6; Conservative
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Best Local Similarity
T; Conserva
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ORGANISM: Human
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SEQ ID NO 2
LENGTH: 370
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                                                                                                                                                                       LENGTH: 361
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APPLICANT: Baumann, Heinz
APPLICANT: Levin, Steven D.
APPLICANT: Levin, Steven D.
APPLICANT: Levin, Steven D.
APPLICANT: Leonard, Warren J.
APPLICANT: Leonard
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Publication No. US20030157118A1
GENERAL INFORMATION:
APPLICANT: Cobezon-Silva, Teresa Elisa Virginia
APPLICANT: Coche, Thierry
APPLICANT: Gaulis, Swann Romain Jean-Thomas
APPLICANT: Casair, Jean-Pol
APPLICANT: Cassart, Jean-Pol
TITLE OF INVENTION: Tumour-Specific Animal Proteins
FILE REFERENCE: BC45300-1
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Patent No. US20020160949A1
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APPLICANT: Ozaki, Katsutoshi
                      PRIOR FILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 77.0-
                                                      NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENCTH: 353
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 66.0
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (227)..(247)
US-09-895-593-3
                                                                                                                                                                                                                                                                 ; NAME/KEY: TRANSMEM
; LOCATION: (227)...(247)
US-09-895-943-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mus musculus
                                                                                                                                                                                                                 ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                    FEATURE
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91 SPHVTGGG 98
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US-10-374-780A-1701
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US-09-895-943-3
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GROWERL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)
FILE REFERENCE: 38-10(52052)
CURRENT APPLICATION WUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10058
LENGTH: 855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 87.5%; Pred. No. 7.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: magnetite-containing magnetic coccus US-10-369-493-10058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OMURA, SATOSHI
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: HORIKAWA, UUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHATORI, WASHIRA
TITLE OF INVERTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                   US-10-369-493-10058
; Sequence 10058, Application US/10369493
; Publication No. US20030233675A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 66.7
Matches 6; Conservative
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                  22 VTGGGAM 28
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LENGTH: 330
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Sequence 3. Application US/09895943

Patent No. US20020668323A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
CHAIR CONTRACTION:
TITLE OF INVENTION: Uses Thereof
TITLE OF INVENTION: Uses Thereof
FILE REPRENCE: 00-514-C
CURRENT APPLICATION NUMBER: US/09/895,943
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: 60/214,866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Orthologous to G1652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR PELING DATE: 2001-08-09
PRIOR PELING DATE: 2001-08-22
PRIOR PEPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-12-11
PRIOR PILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/11,468
PRIOR PILING DATE: 2002-06-19
PRIOR PILING DATE: 2002-08-09
Sequence 1701, Application US/10374780A Publication No. US20040019927A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Pilgrim, Marsha L
Dubell III, Arnold T
Pineda, Omaira
                                                                                                                      Riechmann, Jose Luis
Jiang, Cai-Zhong
Heard, Jacqueline E
                                                                                                                                                                                                                 Haake, Volker
Creelman, Robert A
Ratcliffe, Oliver
Adam, Luc J
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                                                                                             APPLICANT: Sherman, Bradley K
                                                                                                                                                                                                                                                                                                                           Reuber, T. Lynne
Keddie, James
Broun, Pierre E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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Sequence 20821

Sequence 20821, Application US/10369493

Publication No. US20030233675A1

Sublication No. US20030233675A1

GRNERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Blater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldm
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APPLICANT: Gao, Yongwei
APPLICANT: Biater, Seven C.
APPLICANT: Blater, Seven C.
APPLICANT: Slater, Seven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REPERENCE: 38-10 (52052) B
FILE REPERENCE: 38-10 (52052) B
FILE REPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15324
LENGTH: 294
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67.9%; Score 36; DB 15; Length 600;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matchés 6; Conservative 2; Mismatches 1; Indels
Ouery Match
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 15324, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Xanthomonas campestris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 TPRLIGSGS 250
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Sequence 15690, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Goldman, Barry
APPLICANT: Goldman, Barry S.

FILE REFERENCE: 38-10 (52052) B.

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-21

NUMBER: OF SEQ ID NOS: 47374
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US,10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 16082
LENGTH: 276
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                                                                                                                                                                                                                                                                                                        67.9%; Score 36; DB 14; Length 244; 70.0%; Pred. No. 2e+02; tive 0; Mismatches 3; Indels
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                                                                                                                                                                                               , ORGANISM: Streptomyces avermitilis
US-10-156-761-15056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Xanthomonas campestris US-10-369-493-16082
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               PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 15056
LENGTH: 244
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.0°
Matches 7; Conservative
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LENGTH: 276
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APPLICANT: Pern, Sharron G.
APPLICANT: Pern, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hans, David R.
APPLICANT: Hansel, David K.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
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                                                                                                                                                            67.9%; Score 36; DB 14; Length 54; 60.0%; Pred. No. 45; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: MAP TO AL133476.4

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TITLE PERERNCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PLING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 15056, Application US/10156761; Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 27829, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
                                                                             TYPE: PRT; TYPE: PRT; CRGANISM: Streptomyces avermitilis US-10-156-761-13012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UNN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                       Query Match
Best Local Similarity 60.0.
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13012
                                                                                                                                                                                                                                                                                                       :| :|||||:
28 SPYMTGGGAL 37
                                                                                                                                                                                                                                                                        1 TPRVTGGGAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 TPRATGRGA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TPRVTGGGA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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US-10-029-386-27829
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LENGTH: 145
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                                                      LENGTH
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Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                      Query Match

69.8%; Score 37; DB 14; Length 313;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13012. Application US/10156761

PUBLICATION NO. US20030119018A1

GENERAL INFORMATION:
APPLICANT: ONUTA, SATOSHI
APPLICANT: ISTIKAWA, JUN
APPLICANT: ISTIKAWA, JUN
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SATAKI, YOSHIVUKI
APPLICANT: SATAKI, YOSHIVUKI
APPLICANT: ATTORI, MASAHIRA
TITLE OF INVENTION NOVEL POLYNUCLEOTIDES
TITLE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-30

PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HORIEAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
NUMBER OF SEG ID NOS: 15109
SEQ ID NO 12713
LENGTH: 748
                  NUMBER OF SEQ ID NOS: 242
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 12713, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT; CRGANISM: Streptomyces avermitilis US-10-156-761-12713
                                                                                                                                        ) ORGANISM: C. aurantiacus (22971932)
US-10-306-762-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             593 PRINGGGA 600
                                                                                                                                                                                                                                                                                                                                                                98 SPKVTGGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PRVTGGGA 9
                                                                                                                                                                                                                                                                                                                  1 TPRVTGGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-156-761-13012
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 16
US-10-156-761-12713
                                                                        SEQ ID NO 109
                                                                                                                           TYPE: PRT
                                                                                                 LENGTH:
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APPLICANT: Glazebrock, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Goff, Stephen A.
APPLICANT: Karagiri, Fumiyaki
APPLICANT: Krangiri, Fumiyaki
APPLICANT: Moughamer, Todd
APPLICANT: Moughamer, Todd
APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
TITLE OF INVENTION: IDENTIFICATION NUMBER: US/10/259,194A
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/370,433
PRIOR PLING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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73.6%; Score 39; DB 15; Length 665;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.6%; Score 39; DB 15; Length 342; 75.0%; Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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2.10-374-780A-2854
; Sequence 2854, Application US/10374780A
; Publication No. US20040019927A1
PRIOR APPLICATION NUMBER: 60/291,672
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/330,336
PRIOR PILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 60/265,530
PRIOR FILING DATE: 2001-01-31
PRIOR PELING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 269
SOFTWARE: PATCHLIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 124, Application US/10259194A
Publication No. US20040010815A1
GENERAL INFORMATION:
APPLICANT: Lange, Markus B.
APPLICANT: Ghasemian, Majid
APPLICANT: Griggs, Steven P.
APPLICANT: Cooper, Bret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||::||| :
27 TPRLSGGGTL 36
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:||||:
43 PRITGGGS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PRVTGGGA 9
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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Gaps
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APPLICANT: Pilgrim, Marsha L
APPLICANT: Pilgrim, Marsha L
APPLICANT: Pinded. Omaira
APPLICANT: Pinded. Omaira
APPLICANT: Pinded. Omaira
APPLICANT: Pinded. Omaira
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES IN PLANTS
FILE REPERENCE: Mall - 0047 CLP
FILE REPERENCE: Mall - 0047 CLP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT APPLICATION NUMBER: 00/310,847
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-22
PRIOR PILING DATE: 2001-08-22
PRIOR PILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-19
PRIOR FILING DATE: 2002-06-09
PRIOR FILING DATE: 2002-06-09
PRIOR FILING DATE: 2002-08-09
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Publication No. US20030187220A1

GENERAL INFORMATION:
APPLICANT: Park, Frances
APPLICANT: Gajiwala, Ketan S.
APPLICANT: Buchanan, Sean Grant
APPLICANT: Buchanan, Sean Grant
TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF A FLAVIN
TITLE OF INVENTION: MONONUCLECTIDE BINDING PROTEIN (FMNBP)
FILE REFERENCE: 52498-20011.00
CURRENT FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: US 60/334,132

PRIOR FILING DATE: 2001-11-28
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                    APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                     Creelman, Robert A
Ratcliffe, Oliver
Adam, Inc J
Reuber, T. Lynne
Keddie, James
Broun, Pierre E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: G2373
US-10-374-780A-2854
                                                                                                                                                                 Haake, Volker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 TPSVTGGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TPRVTGGG 8
GENERAL INFORMATION:
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US-10-306-762-109
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POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
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APPLICANT: Stone, David J
APPLICANT: Stone, David J
APPLICANT: Stone, David J
APPLICANT: Stone, David J
APPLICANT: Stone, Catherine E
APPLICANT: Burgess, Catherine E
TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES
TITLE OF INVENTION: USING THE SAME
FILE REPERENCE: 12402-245
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: 60/268,595
PRIOR APPLICATION NUMBER: 60/265,306
PRIOR PILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/262,454
PRIOR FILING DATE: 2001-01-18
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PRIOR APPLICATION NUMBER: 60/261,376
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peyman, John A
Gorman, Linda
Mezes, Peter D
Kekuda, Ramesh
Taupier Jr, Raymond J
Gerlach, Valerie
                                                                                                                                                       Sequence 86, Application US/10051874
Publication No. US20040005557A1
GENERAL INFORMATION:
                                                                                                                                                                                                                        APPLICANT: Padigaru, Muralidhara APPLICANT: Alsobrook II, John P APPLICANT: Colman, Stewn D APPLICANT: Spytek, Kimberly A APPLICANT: Boldog, Ferenc APPLICANT: Vernet, Corine AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patturajan, Meera
Shimkets, Richard A
Pena, Carol BA
Tchernev, Velizar T
Zerhusen, Bryan D
Millet, Isabelle
Millet, Charles E
Lepley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baumgartner, Jason C
Herrman, John L
                                                                                                                                                                                                                                                                                                                                                                      Li, Li
Shenoy, Suresh G
Casman, Stacie J
Guo, Xiaojia Sasha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MacDougall, John R
Malyankar, Uriel M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Edinger, Shlomit R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smithson, Glennda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu, Xiaohong
Ellerman, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 269
                             ||:||||:
43 PRITGGGS 50
2 PRVTGGGA 9
                                                                                                                  RESULT 11
US-10-051-874-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
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TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
TITLE OF INVENTION: USING THE SAME
FILE REFERENCE: 21402-245
                                                                                                                                      Gaps
                                                                                                                                      0,
                                                                                                   73.6%; Score 39; DB 15; Length 342; 75.0%; Pred. No. 89; tive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: 60/268,595
PRIOR FILING DATE: 2001-02-14
PRIOR PILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-09-27
PRIOR PILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/262,587
PRIOR APPLICATION NUMBER: 60/202,409
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
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Herrman, John L
Peyman, John A
Gorman, Linda
Mezes, Peter D
Kekuda, Ramesh
Taupier Jr, Raymond J
                                                                                                                                                                                                                                                                                               Sequence 87, Application US/10051874
Publication No. US20040005557A1
GENERAL INPORMATION
APPLICANT: Padigaru, Muralidhara
APPLICANT: Alsobrook II, John P
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Shimkets, Richard A
Pena, Carol EA
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Zerhusen, Bryan D
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Grosse, William M
Liu, Xiaohong
Ellerman, Karen
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Spytek, Kimberly A
Boldog, Ferenc
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MacDougall, John R
Malyankar, Uriel M
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Miller, Charles E
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Smithson, Glennda
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Stone, David J
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Shenoy, Suresh G
Casman, Stacie J
; SEQ ID NO 86
; LENGTH: 342
; TYPE: PT
; ORGANISM: Rattus norvegicus
US-10-051-874-86
                                                                                               Query Match
Best Local Similarity 75.0'
                                                                                                                                                                                                                  43 PRITGGGS 50
                                                                                                                                                                               2 PRVTGGGA 9
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APPLICANT: Elleman, Mark
APPLICANT: Elleman, Mark
APPLICANT: Stone, David J
APPLICANT: Bothenberg, Mark
APPLICANT: Brone, David J
APPLICANT: Brone, David J
APPLICANT: Brone, David J
TITLE OF INVENTION: USING THE SAME
CURRENT APPLICATION NUMBER: 60/268, 595
PRIOR PELLOR DATE: 2001-02-14
PRIOR PELLOR DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/262, 587
PRIOR APPLICATION NUMBER: 60/262, 587
PRIOR PELLOR DATE: 2001-01-18
PRIOR PELLOR DATE: 2001-03-16
PRIOR PELLOR DATE: 2001-10-18
PRIOR PELLOR DATE: 2001-10-18
PRIOR PELLOR DATE: 2001-10-18
PRIOR PELLOR DATE: 2001-01-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.6%; Score 39; DB 15; Length 285; 75.0%; Pred. No. 75;
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CURRENT APPLICATION NUMBER: US/10/109,616
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/280,509
PRIOR PELING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/311,055
PRIOR PELING DATE: 2001-08-08
PRIOR FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10109616
Publication No. US20030167484A1
GENERAL INFORMATION:
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Best Local Similarity 75.04
---- 6; Conservative
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Best Local Similarity 75.v.
...a 6; Conservative
Ellerman, Karen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-051-874-89
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43 PRITGGGS 50
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         CURRENT FILLING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: US/09/692,170C
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-03-27
PRIOR PILING DATE: 2000-03-27
PRIOR PLING DATE: 2000-03-27
PRIOR PLING DATE: 1998-02-11
PRIOR APPLICATION NUMBER: US 09/021,298
PRIOR APPLICATION NUMBER: US 08/950,064
PRIOR PILING DATE: 1998-02-10
PRIOR PILING DATE: 1998-02-10
PRIOR PLING DATE: 1997-10-14
PRIOR FILING DATE: 1997-10-14
PRIOR FILING DATE: 1996-11-12
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 8
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LOCATION: (10)...(10)

COTHER INFORMATION: Xaa = L, F or M
US-10-405-231-8
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Smithson, Glennda
Baumgartner, Jason C
Herrman, John L
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Gerlach, Valerie
Grosse, William M
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APPLICANT: Alsobrook II, John P
APPLICANT: Colman, Steven D
APPLICANT: Spytek, Kimberly A
APPLICANT: Boldog, Ferenc
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Tchernev, Velizar T
Zerhusen, Bryan D
Millet, Isabelle
Miller, Charles E
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Shenoy, Suresh G
Casman, Stacie J
Guo, Xiaojia Sasha
Edinger, Shlomit R
2003-04-03
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Malyankar, Uriel M
Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial sequence
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Kekuda, Ramesh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
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Matches 9; Conserv
CURRENT FILING DATE:
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APPLICANT:
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APPLICANT: Diamond, Don J. TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOWEGALOVIRUS FILE REFERENCE: 1954-346 CURRENT APPLICATION UNMBER: US/10/405,231
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                                                                                                                                                                                                                        vuery match 100.0%; Score 53; DB 14; Length 579; Best Local Similarity 100.0%; Pred. No. 0.68; Matches 10; Conservative 0; Mismatcher
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                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (10); OTHER INFORMATION: Xaa = L, F or M US-10-238-607-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/10238607 Publication No. US20030118602A1 GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                           407 TPRVTGGGAM 416
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Berencei, Klara
Kari, Cabba
TITLE OF INVENTION: No. US20030120060Alel Cytomegalovirus DNA Constructs and
Uses Therefor
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ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PCC compatible
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE: 19-Aug-2002
FILING DATE: 19-Aug-2002
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION: CURKNOWN>
PRIOR APPLICATION NUMBER: US/09/171,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/10223538
Publication No. US20030120060A1
GENERAL INFORMATION:
The Wistar Institute of, Anatomy & Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                        APPLICATION NUMBER: 19,741-1999
FILING DATE: 19-741-1996
APPLICATION NUMBER: US 60/015,717
FILING DATE: 23-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: KOdroff, Cathy A.
REGISTATION NUMBER: WSF66APCT
RELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEPAX: 215-540-9200
TELEPAX: 215-540-9210
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERIFICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: WST66APCT TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19-Jan-1999
APPLICATION NUMBER: US 60/015,717
FILING DATE: 23-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/223,538
FILING DATE: 19-AUG-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/171,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-223-538-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 579 amino acids
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STATE: Pennsylvania
COUNTRY: USA
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Matches 10; Conserv
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TYPE: PRT
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Publication No. US20030190328A1
GENERAL INFORMATION:
APPLICANT: Diamond, Don J.
TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS
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APPLICANT: NICOLette, Charles A.
TITLE OF INVENTION: THERAPEUTIC ANTI-CYTOMEGALOVIRUS
TITLE OF INVENTION: COMPOUNDS
FILE REFERENCE: GZ 209500
CURRENT APPLICATION NUMBER: US/09/812,079A
CURRENT FILING DATE: 2001-03-19
PRIOR PILING DATE: 2000-03-21
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CURRENT APPLICATION NUMBER: US/10/405,231
CURRENT FILING DATE: 2003-04-03
PRIOR FILING DATE: 2000-020
PRIOR PILING DATE: 2000-03-27
PRIOR PLING DATE: 2000-03-27
PRIOR PLING DATE: 2000-03-27
PRIOR PILING DATE: 2000-03-27
PRIOR PLING DATE: 1998-05-11
PRIOR PILING DATE: 1998-05-11
PRIOR FILING DATE: 1998-05-11
PRIOR FILING DATE: 1998-05-10
PRIOR FILING DATE: 1998-02-10
PRIOR PILING DATE: 1998-02-10
PRIOR PILING DATE: 1997-10-14
PRIOR PILING DATE: 1997-10-14
PRIOR PILING DATE: 1997-10-14
PRIOR PILING DATE: 1996-11-12
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PARENTIN VERSION 3.1
LENGTH: 10
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PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 15
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                                                                                                               TYPE: PRT ORGANISM: Human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Human cytomegalovirus
PRIOR FILING DATE: 1996-11-12
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
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nes 10; Conserv
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                                                                   SEQ ID NO 7
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Matches
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TITLE OF INVENTION: No. US20030120060Alel Cytomegalovirus DNA Constructs and Uses Therefor
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UGENERAL INFORMATION

SEQUENCE 2, Application US/10434982

PUBLICATION NO. US20030199673A1

GENERAL INFORMATION:

APPLICANT: Nicolette, Charles A.

TITLE OF INVENTION: THERAPEUTIC ANTI-CYTOMEGALOVIRUS COMPOUNDS

TILE REFERENCE: 5018C

CURRENT APPLICATION NUMBER: US/10/434,982

CURRENT FILING DATE: 2003-05-10

PRIOR PILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: US 60/191,050

PRIOR PILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 2

LENGTH: 561
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                                                                                                                                                              Query Match 100.0%; Score 53; DB 9; Length 561; Best Local Similarity 100.0%; Pred. No. 0.66; Matches 10; Conservative 0; Mismatches 0; Indels
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APPLICANT: The Wistar Institute of, Anatomy & Biology
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COMPUTER: ISM C compatible
SPEATING SYSTEM: PC-DOS/MS-DOS
OPFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0
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ADDRESSEE: Howson and Howson
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Publication No. US20030120060A1
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Berencsi, Klara
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STATE: Pennsylvania
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COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                             ORGANISM: Homo sapiens
                 SEQ ID NO 2
LENGTH: 561
TYPE: PRT
                                                                                                                        US-09-812-079A-2
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Sequence 432, App Sequence 432, App Sequence 432, App	equence 432, equence 432.	equence 432,		equence 432,		432,	432,	432,	432,	432,		432,	432,	432,	432,	432,	432,	432,	equence 432, equence 432	equence 432,	equence 432,	equence 432,	equence 432,	_	equence 432,	equence 432,	432,	_	432,	_	432,	432,	432,	equence 432,									THEREFOR											
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432, App 432, App 432, App		_		_																																																		
Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	eduence	equence	equence	Sequence	Sequence	equence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence						Sequence		Sequence	ednence	equence	ednence	equence		equence	ednence	o d	, ai	ė	e e	e e	, e		e)
US-10-147-490-432 US-10-147-494-432 US-10-147-498-432	J-147-514-43 J-147-524-43)-152-379-43 -152-394-43	0-152-406-43)-156-847-43)-157-799-43	0-160-504-43)-145-634-43)-147-520-43)-157-781-43	1-176-989-43)-147-491-43)-152-379-43)-152-382-43)-152-383-43)-152-384-43)-152-384-43	152-389-43	152-390-43	152-392-43	1-153-756-43 1-157-784-43	157-797-43	1-158-491-43	142-762-43	0-142-764-43)-142-766-43)-145-625-43	145-627-43	145-960-43	145-962-43	-146-789-43 -147-483-43	1-147-496-43	1-147-505-43	1-147-516-43	-152-398-43 -139-980-43	-145-750-43	1-152-373-43	1223-081-13	-121-044-43 -121-055-43	1-121-057-43	-121-058-43 -121-059-43	-121-060-43	123-109-43	-123-154-43 -123-157-43	-123-906-43	-124-814-43	124-816-43	-124-620-43 -125-704-43	1-125-927-43	1-223-082-13)-142-889-43 145 674 43	-143-6/4-43 -147-497-43	1-152-371-43	1-152-374-43	1-152-375-43	-152-3//-43 -152-386-43	-152-391-43	1-152-399-43	5%-9%9-9CT-
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GenCore version 5.1.6
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March 7, 2004, 13:03:22 ; Search time 34 Seconds
 (without alignments)
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		7, Appli	7, Appli	, Appli	2, Appli	6, Appli	8, Appli	8, Appli	8, Appli	89, Appl	2, Appli	86, Appl	87, Appl	124, App	2854, Ap	109, App
	Description	Sequence 7, Appl	Sequence 7,	Sequence 2,	Sequence 2,	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
	ΠD	US-10-238-607-7	US-10-405-231-7	US-09-812-079A-2	US-10-434-982-2	US-10-223-538-6	US-10-223-538-8	US-10-238-607-8	US-10-405-231-8	US-10-051-874-89	US-10-109-616-2	US-10-051-874-86	US-10-051-874-87	US-10-259-194A-124	US-10-374-780A-2854	US-10-306-762-109
	DB	14	14	0	14	14	14	14	14	15	14	15	15	15	15	14
	Query Match Length DB	10	10	561	195	579	579	10	10	285	339	342	342	999	383	313
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	90.6	9.06	73.6	73.6	73.6	73.6	73.6	71.7	8.69
	Score	53	53	53	53	53	53	48	48	39	39	39	39	39	38	37
	Result No.		2	e	4	S	9	7	80	σ	10	11	12	13	14	15

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US-10-156-761-11 US-10-156-761-11 US-10-156-761-11 US-10-156-761-11 US-10-156-761-11 US-10-156-761-11 US-10-156-761-11 US-10-156-493-11 US-10-156-493-11 US-10-156-761-9 US-10-10-10-10-10-10-10-10-10-10-10-10-10-	99-993-6993-6999-9999-9999-9999-9999-99
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